

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:09:50 ; Search time 46 Seconds
(without alignments)
2180.765 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
Sequence: 1 MNVNLNNGRTTICDAYNVVA.....GTQFELNMIMFVTNLPPIY 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3314	100.0	632	22 AAU02021	B. thuringiensis t
2	3048.5	92.0	633	15 AAR56696	CryIIA insecticida
3	3046.5	91.9	635	22 AAU02043	B. thuringiensis t
4	3043.5	91.8	634	21 AAY94259	Cry2Aa delta-endot
5	3015.5	91.0	635	19 AAW75772	Amino acid sequenc
6	3010.5	90.8	633	21 AAY94260	Cry2Ab delta-endot
7	3005.5	90.7	634	21 AAY94254	Cry2Ab delta-endot
8	2974.5	89.8	633	13 AAR20030	Bacillus thuringie
9	2914.5	87.9	633	19 AAW75775	Amino acid sequenc

10	2913.5	87.9	633	19 AAW75774	Amino acid sequenc
11	2610.5	78.8	623	19 AAW75773	Amino acid sequenc
12	2582.5	77.9	625	22 AAU02044	B. thuringiensis t
13	1274.5	38.5	290	9 AAP83002	Sequence of P-2 pr
14	1082	32.6	706	18 AAW31199	Bacillus popilliae
15	499	15.1	99	9 AAP81356	Sequence of fragme
16	336.5	10.2	643	10 AAP91462	67-kD protein toxi
17	336.5	10.2	643	17 AAR97735	Bacillus thuringie
18	331.5	10.0	710	22 AAU02041	B. thuringiensis t
19	327.5	9.9	719	22 AAB66908	Insecticidal prote
20	327.5	9.9	719	22 AAB66911	Insecticidal prote
21	325.5	9.8	719	22 AAB66910	Insecticidal prote
22	325	9.8	718	22 AAB66907	Insecticidal prote
23	325	9.8	719	21 ABB07073	Bacillus thuringie
24	324.5	9.8	719	11 AAR08041	81 kD endotoxin de
25	324.5	9.8	719	22 AAU02095	Bacillus thuringie
26	324.5	9.8	719	22 AAB66909	Insecticidal prote
27	314.5	9.5	1217	22 AAU02092	Bacillus thuringie
28	311.5	9.4	1156	19 AAW46857	Bacillus thuringie
29	311.5	9.4	1156	20 AAY24960	Bacillus thuringie
30	311.5	9.4	1156	22 AAU02034	B. thuringiensis t
31	311	9.4	1157	20 AAW84587	Amino acid sequenc
32	311	9.4	1157	20 AAW84593	Amino acid sequenc
33	310.5	9.4	719	22 AAB66912	Insecticidal prote
34	310	9.4	1157	20 AAW84580	Amino acid sequenc
35	309	9.3	1157	20 AAW84584	Amino acid sequenc
36	309	9.3	1157	20 AAW84590	Amino acid sequenc
37	309	9.3	1157	20 AAW84581	Amino acid sequenc
38	308	9.3	1157	20 AAW84583	Amino acid sequenc
39	308	9.3	1157	20 AAW84588	Amino acid sequenc
40	308	9.3	1157	20 AAW84589	Amino acid sequenc
41	308	9.3	1157	20 AAW84592	Amino acid sequenc
42	307	9.3	1138	15 AAR46225	Bacillus thuringie
43	307	9.3	1157	15 AAR48678	Insecticidal proto
44	307	9.3	1157	20 AAW84582	Amino acid sequenc
45	307	9.3	1157	20 AAW84586	Amino acid sequenc

ALIGNMENTS

RESULT 1

AAU02021

ID AAU02021 standard; Protein; 632 AA.

XX AAU02021;

AC AAU02021;

XX 29-AUG-2001 (first entry)

DT 29-AUG-2001 (first entry)

XX B. thuringiensis toxic crystal protein, CryET31.

DE Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
transgenic plant; corn; wheat; soybean; oat; cotton; rice; sorghum;
sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
cotton leaf perforator; CryET31.

XX Bacillus thuringiensis.

OS WO200119859-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US25361.

XX 15-SEP-1999; 99US-0153995.

XX (MONS) MONSANTO CO.

XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;

XX WPI; 2001-281518/29.

DR N-PSDB; AAS02464.

XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides

PT and the polynucleotides that encode them, useful for increasing the

PT insect resistance of plant -

XX

PS Claim 5; Page 102-103; 173pp; English.

XX

CC The sequence represents a B. thuringiensis Lepidopteran-active

CC delta-endotoxin, crystal protein CryET31. The Lepidopteran-active B.

CC thuringiensis delta-endotoxin polypeptides may be used as compositions

CC that are applied to plant crops to protect them from insect damage. The

CC polynucleotides may be used in the production of transgenic plants that

CC express the insecticidal polypeptides and consequently have improved

CC insect resistance compared to non-transformed plants. Monocotyledonous or

CC dicotyledonous plants may be protected in this way, for example corn,

CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,

CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,

CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree

CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,

CC cotton leaf perforator and spruce budworm) may be affected by application

CC of the insecticidal polypeptides (full details given in specification).

XX

SQ Sequence 632 AA;

Query Match 100.0%; Score 3314; DB 22; Length 632;

Best Local Similarity 100.0%; Pred. No. 3.7e-259;

Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKS LDTIRKEWMEWKRTDHSLYVAPIVGTVSSF 60

Db 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKS LDTIRKEWMEWKRTDHSLYVAPIVGTVSSF 60

QY 61 LLKKVGS LIGKRILSELWGLIFPSSGSTNMQDLRETEQFLNQLRNTDTLARVNAELEG 120

Db 61 LLKKVGS LIGKRILSELWGLIFPSSGSTNMQDLRETEQFLNQLRNTDTLARVNAELEG 120

QY 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA 180

Db 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVVLNADWGISATLRTYQNYLKNYTTSEYNYCINTYQTAFGLNTRLHD 240

Db 181 ANMHLSFIRDVVLNADWGISATLRTYQNYLKNYTTSEYNYCINTYQTAFGLNTRLHD 240

QY 241 MLEFRTYMFNLVFEYVSWLSFKYQSLLVSSGANLYASGSGPQQTQSFSDWPFLYSLF 300

Db 241 MLEFRTYMFNLVFEYVSWLSFKYQSLLVSSGANLYASGSGPQQTQSFSDWPFLYSLF 300

QY 301 QVNSNYVLNGFSGARLTQTFPNIGGLPGTTTTTHALLAARVNYSGVSSGDIGAVFNQNF 360

Db 301 QVNSNYVLNGFSGARLTQTFPNIGGLPGTTTTTHALLAARVNYSGVSSGDIGAVFNQNF 360

QY 361 CSTFLPPLLTFFVRSWLDGSDRGVNTVTNNWQTESFESTLGLRCGAFARGNSNYFPDY 420

Db 361 CSTFLPPLLTFFVRSWLDGSDRGVNTVTNNWQTESFESTLGLRCGAFARGNSNYFPDY 420

QY 421 FIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYAVHENG 480

Db 421 FIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYAVHENG 480

QY 481 TWIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 540

Db 481 TWIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 540

QY 541 SYNLYLRVSSLGNSITRVINGRVTYASNVNTTNDGVNDNGARFLDINMGNVVSDNT 600

Db 541 SYNLYLRVSSLGNSITRVINGRVTYASNVNTTNDGVNDNGARFLDINMGNVVSDNT 600

QY 601 NVPLDINVTNFSGTQFELMNMIFVPTNLPIY 632

Db 601 NVPLDINVTNFSGTQFELMNMIFVPTNLPIY 632

RESULT 2

AAR56696

ID AAR56696 standard; Protein; 633 AA.

XX

AC AAR56696;

XX

DT 25-MAR-2003 (updated)

DT 27-MAR-1995 (first entry)

XX

DE CryIIA insecticidal crystal protein.

XX

KW CryIIA; CryIIIA; CryIIB; CryC; P-2; CryBI; insecticidal protein crystal;

KW lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;

KW probe; hybridisation.

XX

OS Bacillus thuringiensis.

XX

PN US5338544-A.

XX

PD 16-AUG-1994.

XX

PF 26-FEB-1993; 93US-0023736.

XX

PR 16-APR-1987; 87US-0039542.

PR 11-JUL-1989; 89US-0379015.

PR 28-AUG-1991; 91US-0751452.

PR 26-FEB-1993; 93US-0023736.

XX

PA (ECOG-) ECOGEN INC.

XX

PI Donovan WP;

XX

DR WPI; 1994-263236/32.

DR N-PSDB; AAQ71025.

XX

PT New Cry IIB protein - obtd. from the cry II B gene in Bacillus

PT thuringiensis var. Kurstaki, active against lepidopteran insects

XX

PS Example 2; Fig 2A-2C; 39pp; English.

XX

CC This sequence shows the amino acid sequence of CryIIA protein.

CC The CryIIA gene was used as a probe to identify CryIIA related

CC sequences, ie. CryIIB. CryIIB encodes an insecticidal crystal

CC protein isolated from Bacillus thuringiensis var. kurstaki. It

CC produces crystal proteins during sporulation which are specifically

CC toxic to certain orders and species of insects, esp. lepidopterans.

CC CryIIB can be used in compositions used as environmentally acceptable

CC insecticides. (See also AAR56697-8)

CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 633 AA;

Query Match 92.0%; Score 3048.5; DB 15; Length 633;

Best Local Similarity 90.7%; Pred. No. 1.1e-237;

Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

QY 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKS LDTIRKEWMEWKRTDHSLYVAPIVGTVSSF 60

Db 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKS LDTIRKEWMEWKRTDHSLYVAPIVGTVSSF 60

QY 61 LLKKVGS LIGKRILSELWGLIFPSSGSTNMQDLRETEQFLNQLRNTDTLARVNAELEG 120

Db 61 LLKKVGS LIGKRILSELWGLIFPSSGSTNMQDLRETEQFLNQLRNTDTLARVNAELEG 120

QY 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA 180

Db 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVVLNADWGISATLRTYQNYLKNYTTSEYNYCINTYQTAFGLNTRLHD 240

Db 181 ANMHLSFIRDVVLNADWGISATLRTYQNYLKNYTTSEYNYCINTYQTAFGLNTRLHD 240

KW Lepidopteran; Dipteran; plastid transit peptide; PTP; insecticidal;
KW plaid targeting peptide.
XX
OS Bacillus thuringiensis.
XX
PN WO200026371-A1.
XX
PD 11-MAY-2000.
XX
XX 04-NOV-1999; 99WO-US26086.
XX
XX 04-NOV-1998; 98US-0186002.
XX
PA (MONS) MONSANTO CO.
XX
XX Corbin DR, Romano CP;
PI
XX
DR WPI; 2000-376130/32.
DR N-PSDB; AAA15561.
XX
XX
PT New method of expressing insecticidal proteins in plants transformed
PT with a Bacillus thuringiensis delta-endotoxin encoding gene resulting
PT in effective control of susceptible target pests -
XX
PS Claim 14; Page 86-87; 104pp; English.
XX
CC The present sequence is cry2Aa delta-endotoxin protein. Delta-endotoxins
CC are produced by Bacillus thuringiensis during sporulation. These proteins
CC are toxic to certain species of insect e.g. Lepidopteran and Coleopteran
CC larvae. An insect-resistant transgenic plant has been constructed which
CC contains the present sequence. The cry2Aa gene would be transferred into
CC plants via expression vectors, which subsequently allow high expression
CC of the cry2Aa gene. The present sequence lacks Dipteran inhibitory
CC activity. Protection may be attained against insects such as Ostrina
CC spp., Diatraea spp., Helicoverpa spp., and Spodoptera spp., in Zea mays;
CC Heliothis virescens, Helicoverpa spp., Pectinophora spp., in Gossypium
CC hirsutum; Anticarsia spp., Pseudoplusia spp., Epinotia spp., in Glycine
CC max; and Scirpophaga incertulas in Oryza sativa. Expression of the
CC cry2Aa gene by a plant cell produces a fusion protein comprising
CC an amino-terminal plastid transit peptide (PTP) covalently linked to the
CC delta-endotoxin. The fusion protein functions to localise the
CC delta-endotoxin to a subcellular organelle or compartment.
XX
SQ Sequence 634 AA;

Query Match 91.8%; Score 3043.5; DB 21; Length 634;
Best Local Similarity 90.7%; Pred. No. 2.8e-237;
Matches 573; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

QY 2 NNVLNNGRTTICDAYNVVAHDPSFEHKSLSLTIRKEWMEWKRTDHSLYVAPIVGTSSFL 61
DB 3 NNVLNNGRTTICDAYNVVAHDPSFEHKSLSLTIRKEWMEWKRTDHSLYVAPIVGTSSFL 62
QY 62 LKKVGLIGKRIISLWGLIFPSGGSTNLMQDILRETEQFLNQLRNTDTLARVNAELEGLO 121
DB 63 LKKVGLIGKRIISLWGLIFPSGGSTNLMQDILRETEQFLNQLRNTDTLARVNAELEGLO 122
QY 122 ANIREFNQVDNFINPTQNPVPLSITSSVNTMQQLFNRLPQFRVQGYQLLLPLFAQAA 181
DB 123 ANIREFNQVDNFINPTQNPVPLSITSSVNTMQQLFNRLPQFRVQGYQLLLPLFAQAA 182
QY 182 NMHLSFIRDVVLNADEWGISAAATLRTYQNLKNTTEYSNYCINTYQAFRGLNTRLHDM 241
DB 183 NMHLSFIRDVVLNADEWGISAAATLRTYQNLKNTTEYSNYCINTYQAFRGLNTRLHDM 242
QY 242 LEFRYTMFLNVFEYVSIWSLFKYQSLVSSGANLYASGGPQQQTQSFTSQDWPFLYSLFQ 301
DB 243 LEFRYTMFLNVFEYVSIWSLFKYQSLVSSGANLYASGGPQQQTQSFTSQDWPFLYSLFQ 302
QY 302 VNSNYVLNGFSGARLTQTTFNIGLPGTTTHALLAARVNSYGGVSSGDIQAV-FNQNFS 360
DB 303 VNSNYILSGISGRISITFPNIGLPGTTHSLNSARVNSYGGVSSGLIGATNLNHNFN 362

QY 361 CSTFLPPLLTPEVRSWLDGSDRGVNTVTNMQTESFESTLGRCCGAFARGNSNYFPDY 420
DB 363 CSTVLPPLSTPEVRSWLDGSDRGVNTVTNMQTESFESTLGRCCGAFARGNSNYFPDY 422
QY 421 FIRNISCVPVLVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
DB 423 FIRNISCVPVLVRNEDLRPLHYNQIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 482
QY 481 TMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTARYTLRGNGN 540
DB 483 TMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTARYTLRGNGN 542
QY 541 SYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTNNDGVNDNGARFILDINMGVNVASDNT 600
DB 543 SYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTNNDGVNDNGARFILDINMGVNVASDNT 602
QY 601 NVPLDINVTNFGSTQFELMNMIFVPTNLPPIY 632
DB 603 NVTLDINVTNFGSTQFELMNMIFVPTNLPPIY 634

RESULT 5
AAW75772
ID AAW75772 standard; Protein; 635 AA.
XX
AC AAW75772;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of lepidoteran-active 192M4 toxin.
XX
KW 192M4 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe;
KW lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;
KW Helicoverpa zea; hybridisation.
XX
OS Bacillus thuringiensis.
XX
PN WO9840490-A1.
XX
PD 17-SEP-1998.
XX
PF 13-MAR-1998; 98WO-US05081.
XX
PR 13-MAR-1997; 97US-0040512.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Muller-Cohn J, Narva KE, Schnepf HE;
XX
DR WPI; 1998-506734/43.
DB N-PSDB; AAV52609.
XX
PT New insecticidal Bacillus thuringiensis toxins - useful for
PT controlling lepidopteran pests, especially Ostrinia nubilalis,
PT Heliothis virescens and Helicoverpa zea
XX
PS Claim 5; Pages 25-27; 50pp; English.
XX
CC This is the amino acid sequence of a novel Bacillus thuringiensis toxin
CC used in the method of the invention, to control lepidopteran pests.
CC The new toxins are useful as pesticides, especially for the control of
CC Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The
CC polynucleotide coding sequences are useful for recombinant expression
CC of the toxins and the primers, together with probes derived from the
CC new sequences, are useful for the identification and characterisation
CC of novel genes that encode pesticidal toxins.
XX
SQ Sequence 635 AA;

Query Match 91.0%; Score 3015.5; DB 19; Length 635;
Best Local Similarity 90.2%; Pred. No. 5.2e-235;
Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;


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QY 1 MNNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTIRKEMWKRTHDLSLYVAPIVGTVSSF 60
Db 1 MNNVLNSGRTTICDAYNVVAHDPPSFSEHKSLDTIQEEMWKRTHDLSLYVAPVGTVSSF 60

QY 61 LLKKVGSLLGKRILSELWGLIFPSSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELEG 120
Db 61 LLKKVGSLLGKRILSELWGLIFPSSGSTNLMQDILRETEQFLNQRLNTDTLDRVNAELEG 120

QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFNLRLPQFIQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVVLNADEWGISAATLRTYQNYLKNYTEYSNYCINTYQTAFRLNTRLHD 240
Db 181 ANMHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRLNTRLHD 240

QY 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300

QY 301 QVNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYILSGISGNRLSTTFPNIGGLPGSTTIHLSNARVNYSGVSSGLIGATNLNHF 360

QY 360 SCSTFLPPLLTTPFVRSWLDGSDRGGVNTVTNWQTESFESTLGLRCGA--FTARGNSNYF 417
Db 361 NCSTVLPLLTTPFVRSWLDGSDTREGVATSTTWQTESFQITSGRLRCGAFPFARGNSNYF 420

QY 418 PDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVH 477
Db 421 PDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYMVSVHNRKNNIYAAH 480

QY 478 ENGTMHILAPEDYTGTTFISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRG 537
Db 481 ENGTMHILAPEDYTGTTFISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRG 540

QY 538 NGNSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVAS 597
Db 541 NGNSYNLYLRVSSLGNSTIRVTINGRVYTVPNVTNTNNDGVNDGIDNGARFSDINIGNVAS 600

QY 598 DNTNVPLDINVTENSQTQFELMNMIFVPTNLPPY 632
Db 601 DNTNVPLDINGTLSSGQTQFELMNMIFVPTNLPPY 635

RESULT 6
ID AAY94260
AC AAY94260;
XX AAY94260;
DT 28-JUL-2000 (first entry)
DE Cry2Ab delta-endotoxin.
XX Transgenic plant; insect resistance; cry2Ab delta-endotoxin; Coleopteran;
KW Lepidopteran; Dipteran; plastid transit peptide; PTP; insecticidal;
KW plastid targeting peptide.
XX Bacillus thuringiensis.
OS
XX WO200026371-A1.
PN
XX 11-MAY-2000.
PD
XX 04-NOV-1999; 99WO-US26086.
XX
PR 04-NOV-1998; 98US-0186002.
XX
PA (MONS ) MONSANTO CO.
XX
PI Corbin DR, Romano CP;
XX
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DR WPI; 2000-376130/32.
DR N-PSDB; AAA15566.
XX
PT New method of expressing insecticidal proteins in plants transformed
PT with a Bacillus thuringiensis delta-endotoxin encoding gene resulting
PT in effective control of susceptible target pests -
XX
PS Claim 14; Page 100-101; 104pp; English.
XX
CC The present sequence is the Cry2Ab delta-endotoxin. Delta-endotoxins are
CC produced by Bacillus thuringiensis during sporulation. These proteins are
CC toxic to certain species of insect e.g. Lepidopteran and Coleopteran
CC larvae. An insect-resistant transgenic plant has been constructed which
CC contains the cry2Ab gene. The cry2Ab gene would be transferred into
CC plants via expression vectors, which subsequently allow high expression
CC of the cry2Ab gene. The present sequence lacks Dipteran inhibitory
CC activity. Protection may be attained against insects such as Ostrina
CC spp., Diatraea spp., Helicoverpa spp., and Spodoptera spp., in Zea mays;
CC Heliothis virescens, Helicoverpa spp., Pectinophora spp., in Gossypium
CC hirsutum; Anticarsia spp., Pseudoplusia spp., Epinotia spp., in Glycine
CC max; and Scirpophaga incertulas in Oryza sativa. Expression of the
CC cry2Ab gene by a plant cell produces a fusion protein comprising
CC an amino-terminal plastid transit peptide (PTP) covalently linked to the
CC delta-endotoxin. The fusion protein functions to localise the
CC delta-endotoxin to a subcellular organelle or compartment.
XX
SQ Sequence 633 AA;
```

```
Query Match 90.8%; Score 3010.5; DB 21; Length 633;
Best Local Similarity 89.7%; Pred. No. 1.3e-234;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 1 MNNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTIRKEMWKRTHDLSLYVAPIVGTVSSF 60
Db 1 MNSVLNSGRTTICDAYNVVAHDPPSFQHKSLDTVQKEWTEWKNHSLYLDPIVGTVASP 60

QY 61 LLKKVGSLLGKRILSELWGLIFPSSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELEG 120
Db 61 LLKKVGSLLGKRILSELRLNLIFFPSGSTNLMQDILRETEKFLNQRLNTDTLARVNAELTGL 120

QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNLFNPNRNAVPLSITSSVNTMQQLFNLRLPQFMQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVVLNADEWGISAATLRTYQNYLKNYTEYSNYCINTYQTAFRLNTRLHD 240
Db 181 ANHLSPFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQSAFKGLNTRLHD 240

QY 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300

QY 301 QVNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYVLNGFSGARLNTFPNIVGLPGSTTTTHALLAARVNYSGGISGDIASPFNQNF 360

QY 360 SCSTFLPPLLTTPFVRSWLDGSDRGGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTFLPPLLTTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFARGNSNYFPD 420

QY 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGRAYMVSVHNRKNNIHAVHEN 480

QY 480 GTMIHLAPEDYTGTTFISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNG 539
Db 481 GSMIHLAPNDYTGTTFISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNTTARYTLRGNG 540

QY 540 NSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDN 599
Db 541 NSYNLYLRVSSIGNSTIRVTINGRVYTATNVNTTNDGVNDNGARFSDINIGNVVASN 600

QY 600 TNVPLDINVTENSQTQFELMNMIFVPTNLPPY 632
```


Db 541 NSYNLYRVSSIGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARESDINIGNVVASSN 600

Qy 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPIY 632

Db 601 SDVPLDINVTLSGTQFELNMIMLVPTNISPLY 633

RESULT 10

AAW75774

ID AAW75774 standard; Protein; 633 AA.

XX

AC AAW75774;

XX

DT 02-DEC-1998 (first entry)

XX

DE Amino acid sequence of lepidoteran-active HD525 toxin.

XX

KW HD525 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe;

KW lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;

KW Helicoverpa zea; hybridisation.

XX

OS Bacillus thuringiensis.

XX

PN WO9840490-A1.

XX

PD 17-SEP-1998.

XX

PF 13-MAR-1998; 98WO-US05081.

XX

PR 13-MAR-1997; 97US-0040512.

XX

PA (MYCO) MYCOGEN CORP.

XX

PI Muller-Cohn J, Narva KE, Schnepf HE;

XX

DR WPI; 1998-506734/43.

DR N-PSDB; AAV52611.

XX

XX New insecticidal Bacillus thuringiensis toxins - useful for

PT controlling lepidopteran pests, especially Ostrinia nubilalis,

PT Heliothis virescens and Helicoverpa zea

XX

PS Claim 14; Pages 32-34; 50pp; English.

XX

CC This is the amino acid sequence of a novel Bacillus thuringiensis toxin

CC used in the method of the invention, to control lepidopteran pests.

CC The new toxins are useful as pesticides, especially for the control of

CC Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The

CC polynucleotide coding sequences are useful for recombinant expression

CC of the toxins and the primers, together with probes derived from the

CC new sequences, are useful for the identification and characterisation

CC of novel genes that encode pesticidal toxins.

XX

SQ Sequence 633 AA;

Query Match 87.9%; Score 2913.5; DB 19; Length 633;

Best Local Similarity 87.2%; Pred. No. 9.1e-227;

Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;

Qy 1 MNVNLNNGRTTICDAYNVVAHDPFSEHKSLDTRKEWNEWKRTDHSLSYVAPIGTVSSSF 60

Db 1 MNVNLNNGRTTICDAYNVVVDHDPFSEHKSLDTRKEWNEWKDNHLSLYVDPIGTVASF 60

Qy 61 LLKKVGSLLIGKRIKILSELWGLIPFSGSTNMQDILRETEQFLNQLRNTDTTLARVNAELEG 120

Db 61 LLKKLGSLLIGKRIKILSELRLNLIIPFSGSTNLMEDILRETEKFLNQLNTDTLSRVNAELTGL 120

Qy 121 QANIREFNQQVDNFLNPTQNPVPLSITSSVNTMQQLNRLPQFRVQGYQLLLPLFAQA 180

Db 121 QANVEEFNRQVDNFLNPNRNVAPLSITSSVNTMQQLNRLSQFMQGYQLLLPLFAQA 180

Qy 181 ANMHLSFIRDVVLNADENGISAATLRTYQNYLKNYTTESNYCINTYQTAFRGLNTRLHD 240

Db 181 ANLHLSFIRDVILNAEEWGISAATLRTYQNHRLNRYTRDYSNYCIDTYQTAFRGLNTRLHD 240

Qy 241 MLEFRTYMFNLNVEYVSIWSLFKYQSLLVSSCANLYASGGPQQTQSFTSQDWPFYSLF 300

Db 241 MLEFRTYMFNLNVEYVSIWSLFKYQSLLVSSCANLYASGGPQQTQSFTSQDWPFYSLF 300

Qy 301 QVNSNYVLNGFSGARLTQTFFNIGGLPGTTTHALLAARVNSGGVSSGDI-GAVFNQNF 359

Db 301 QVNSNYVLNGFSGASLFTTFFNIGGLPGSTTTQALLAARVNSGGITSGSGSNFNQNF 360

Qy 360 SCSTFLPPLLTFFVRSWLDSDGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPD 419

Db 361 NCNTISPPLSTSFVRIWLDSDGSDRGVNTVTNWQTESFESTLGLRCGAFPRGNSNYYPG 420

Qy 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYIYAVHEN 479

Db 421 YFIRNISGVSLVLRNEDLKRPLYNEKRNIESPSGTPGGARAYMVSVHNRKNYIYAVHEN 480

Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNRTARYTLRGNG 539

Db 481 GTMIHLAPEDNTGFTISPIHATQVNNQTRTFISEKFGNQSDSLRFEQSNRTARYTLRGNG 540

Qy 540 NSYNLYLRVSSLGNSITRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASSDN 599

Db 541 NSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNVVASSN 600

Qy 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPIY 632

Db 601 SDVPLDINVTLSGTQFELNMIMLVPTNLPIY 633

RESULT 11

AAW75773

ID AAW75773 standard; Protein; 623 AA.

XX

AC AAW75773;

XX

DT 02-DEC-1998 (first entry)

XX

DE Amino acid sequence of lepidoteran-active HD573 toxin.

XX

KW HD573 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe;

KW lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;

KW Helicoverpa zea; hybridisation.

XX

OS Bacillus thuringiensis.

XX

PN WO9840490-A1.

XX

PD 17-SEP-1998.

XX

PF 13-MAR-1998; 98WO-US05081.

XX

PR 13-MAR-1997; 97US-0040512.

XX

PA (MYCO) MYCOGEN CORP.

XX

PI Muller-Cohn J, Narva KE, Schnepf HE;

XX

DR WPI; 1998-506734/43.

DR N-PSDB; AAV52610.

XX

PT New insecticidal Bacillus thuringiensis toxins - useful for

PT controlling lepidopteran pests, especially Ostrinia nubilalis,

PT Heliothis virescens and Helicoverpa zea

XX

PS Claim 14; Pages 28-30; 50pp; English.

XX

CC This is the amino acid sequence of a novel Bacillus thuringiensis toxin

CC used in the method of the invention, to control lepidopteran pests.

CC The new toxins are useful as pesticides, especially for the control of

CC Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The



CC polynucleotide coding sequences are useful for recombinant expression
CC of the toxins and the primers, together with probes derived from the
CC new sequences, are useful for the identification and characterisation
CC of novel genes that encode pesticidal toxins.

XX
SQ Sequence 623 AA;

Query Match 78.8%; Score 2610.5; DB 19; Length 623;
Best Local Similarity 80.3%; Pred. No. 2.9e-202;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSF 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSF 60

QY 61 LLKKVGLIGKRIKILSELWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEG 120
Db 61 LLKKVGLVGRILSELQNLIFPSGSIDLMOEILRATEQFINQRLNADTLGRVNAELAGL 120

QY 121 QANIREFNQVDNPNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVAEFNRQVDNPNPNQNPVPLAIDSNTLQQLFLSRLPQFIQGYQLLLPLFAQA 180

QY 181 ANMHLSPIRDVLNADWEGISAATLRTYQNYLKNYTTSEYNYCINTYQTAFGLNTRLHD 240
Db 181 ANLHLSFIRDVLNADWEGISAATVTRTDHRLNFTRDYSNYCINTYQTAFGLNTRLHD 240

QY 241 MLEFRTYMFLNVFEYVSIWLSFKYQSLVSSGANLYASGGPQQTQSFTSDWPFLYSLF 300
Db 241 MLEFRTYMFLNVFEYVSIWLSFKYQSLVSSGANLYASGGP--TQSFTAHNWPFLYSLF 298

QY 301 QVNSNYVLNGFSGARLTQTFFNIGGLPGTTTTHALLAARVNVSGVSSGDIG-AVFNQNF 359
Db 299 QVNSNYVLNGLSGARTTITFPNIGGLPGSTTTTTLHFAFINRVGGVSSSRIGQANLNQNF 358

QY 360 SCSTFLPPLLTTPFVRSWLDGSDRGGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 359 NISTLFNPLQTPFIRSWLDGSDRGVATSTNWQSGAFETTL-LRFSIFSARGNSNFFPD 417

QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 418 YFIRNISGVGTISNADLARPLHNEIRDI----GTTA--VASLVTVHNRKNNIYDTHEN 471

QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNRTARYTLRGNG 539
Db 472 GTMIHLAPNDYTGFTVSPHATQVNNQIRTFISEKYGNGQDGLRFEQSNRTARYTLRGNG 531

QY 540 NSYNLYLRVSSLSGNTIRVTINGRVYTA-SVNTTNNNDGVNDNGARFELDINMGVNVASDN 599
Db 532 NSYNLYLRVSSLSGNTIRVTINGRVYTA-NVNTTNNNDGVLDNGARFESDINIGNVVASAN 590

QY 600 TNVPLDINVTNFGTQFELNMIMFVPTNLPPIY 632
Db 591 TNVPLDIQVTENGPNQFELNMIMFVPTNPSPLY 623

RESULT 12
AAU02044
ID AAU02044 standard; Protein; 625 AA.

XX
AC AAU02044;
XX
DT 29-AUG-2001 (first entry)
XX

DE B. thuringiensis toxic crystal protein, CryET73.
KW Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET73.
XX

OS Bacillus thuringiensis.
XX
PN WO200119859-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US25361.
XX
PR 15-SEP-1999; 99US-0153995.
XX
PA (MONS) MONSANTO CO.
XX
PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupa MJ;
XX
DR WPI; 2001-281518/29.
DR N-PSDB; AAS02487.
XX
PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
PT and the polynucleotides that encode them, useful for increasing the
PT insect resistance of plant -
XX
PS Claim 5; Page 163-164; 173pp; English.
XX
CC The sequence represents a B. thuringiensis Lepidopteran-active
CC delta-endotoxin, crystal protein CryET73. The Lepidopteran-active B.
CC thuringiensis delta-endotoxin polypeptides may be used as compositions
CC that are applied to plant crops to protect them from insect damage. The
CC polynucleotides may be used in the production of transgenic plants that
CC express the insecticidal polypeptides and consequently have improved
CC insect resistance compared to non-transformed plants. Monocotyledonous or
CC dicotyledonous plants may be protected in this way, for example corn,
CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC cotton leaf perforator and spruce budworm) may be affected by application
CC of the insecticidal polypeptides (full details given in specification).
XX
SQ Sequence 625 AA;

Query Match 77.9%; Score 2582.5; DB 22; Length 625;
Best Local Similarity 80.7%; Pred. No. 5.3e-200;
Matches 503; Conservative 44; Mismatches 65; Indels 11; Gaps 6;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSF 60
Db 1 MNTVLNNGRTTICAHNVVAHDPFSEHKSLNTEKEWKEWKRTDHSLYVAPIVGTVSF 60

QY 61 LLKKVGLIGKRIKILSELWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEG 120
Db 61 LLKKVGLVGRILSELQNLIFPSGSIDLMOEILRATEQFINQRLNADTLGRVNAELAGL 120

QY 121 QANIREFNQVDNPNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVAEFNRQVDNPNPNQNPVPLAIDSNTLQQLFLSRLPQFIQGYQLLLPLFAQA 180

QY 181 ANMHLSPIRDVLNADWEGISAATLRTYQNYLKNYTTSEYNYCINTYQTAFGLNTRLHD 240
Db 181 ANLHLSFIRDVLNADWEGISAATVTRTDHRLNFTRDYSNYCINTYQTAFGLNTRLHD 240

QY 241 MLEFRTYMFLNVFEYVSIWLSFKYQSLVSSGANLYASGGPQQTQSFTSDWPFLYSLF 300
Db 241 MLEFRTYMFLNVFEYVSIWLSFKYQSLVSSGANLYASGGP--TQSFTAHNWPFLYSLF 298

QY 301 QVNSNYVLNGFSGARLTQTFFNIGGLPGTTTTHALLAARVNVSGVSSGDIG-AVFNQNF 359
Db 299 QVNSNYVLNGLSGARTTITFPNIGGLPGSTTTTTLHFAFINRVGGVSSSRIGQANLNQNF 358

QY 360 SCSTFLPPLLTTPFVRSWLDGSDRGGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 359 NISTLFNPLQTPFIRSWLDGSDRGVATSTNWQSGAFETTL-LRFSIFSARGNSNFFPD 417

QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479

Db 418 YFIRNIGVVGTISNADLAPLHNEIRDI---GTTA--VASLVTVHNRKNNIYDTHEN 471
Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDSLRFEQSNNTARTYLRGNG 539
Db 472 GTMIHLAPNDYTGFTVSPHATQVNNQIRTFISEKYGNQDSLRFELSNNTARTYLRGNG 531
Qy 540 NSYNLYRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGVNVASDN 599
Db 532 NSYNLYRVSSIGSSTIRVTINGRVYTA-NVNTTTNDGVLDNGARFSDINIGNVVASAN 590
Qy 600 TNVPLDINVTENSGTQFELMNMIM 622
Db 591 TNVPLDIQVTENDNPQFELMNMIM 613

RESULT 13

AAP83002
ID AAP83002 standard; protein; 290 AA.

XX AAP83002;

XX 12-JAN-1991 (first entry)

DE Sequence of P-2 protein of *Bacillus thuringiensis* var. *kurstaki*.

XX Insecticide; lepidoptera; diptera; P-2 delta-endotoxin;

KW parasporal crystal protein.

XX *Bacillus thuringiensis*.

XX WO8808034-A.

XX 20-OCT-1988.

PF 07-APR-1988; 88WO-US01132.

XX 16-APR-1987; 87US-0039542.

XX (ECOG-) ECOGEN INC.

PA Donovan WP;

XX WPI; 1988-307569/43.

DR N-PSDB; AAN80591.

XX *Bacillus thuringiensis* P-2 toxic gene and expressed protein -

PT used in insecticidal compns. having activity against

PT lepidoptera and diptera insects

XX Claim 10; Fig 2(1) and Fig 2(3); 66pp; English.

CC A gene for *Bacillus thuringiensis* (B.t) P-2 toxin having the DNA
CC sequence specified in Fig 2 (AAN80591), or any portion or deriv. of it,
CC is claimed. Also claimed is the protein encoded by the gene, having the
CC corresponding specified AA sequence in AAP83002. In isolating the P-2
CC gene, the P-2 protein was purified from a donor strain of B.t var.
CC *kurstaki* and the partial AA sequence of the P-2 protein was determined.
CC P-2 gene-specific oligo probe (AAN80590) was synthesised based on the AA
CC sequence. The P-2 toxin encoded by the cloned gene has insecticidal
CC activity against lepidoptera and diptera insects.

CC N.B. The DNA/protein sequence in AAN80591/P83002 is as given in the
CC specifications and is missing bases 901-1800 and the corresp. AAs.

XX Sequence 290 AA;

SQ Query Match 38.5%; Score 1274.5; DB 9; Length 290;

Best Local Similarity 46.2%; Pred. No. 1.1e-94;

Matches 271; Conservative 13; Mismatches 3; Indels 299; Gaps 1;

Qy 1 MNVNLNNGRTTICDAYNVVAHDPPFSFEHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSF 60

Db 1 MNVNLNNGRTTICDAYNVVAHDPPFSFEHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSF 60

Qy 61 LLKKVGLIGRIILSELWGLIFPSSGSTNLMDILRETEQFLNQRNLNTDTLARVNAELEG 120
Db 61 LLKKVGLIGRIILSELWGLIFPSSGSTNLMDILRETEQFLNQRNLNTDTLARVNAELEG 120
Qy 121 QANIREFNQVDNPLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNQVDNPLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Qy 181 ANMHLSFIRDVVLNADWEGISAAATLRTYQNLKNTTTEYSNYCINTYQTAFFGLNTRLHD 240
Db 181 ANMHLSFIRDVVLNADWEGISAAATLRTYQNLKNTTTEYSNYCINTYQTAFFGLNTRLHD 240
Qy 241 MLEFRTYMFNVEYVSIWSLFKYQSLVSSCANLYASGSGPQQTQSFTSQDWPFPLYSLF 300
Db 241 MLEFRTYMFNVEYVSIWSLFKYQSLVSSCANLYASGSGPQQTQSFTSQDWPFPLYSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTFPNIGGLPGTTTHALLAARVNSGGVSSGDIGAVFNQNF 360
Db 249 ----- 248
Qy 361 CSTFLPPLLTFFVRSWLDSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDY 420
Db 249 ----- 248
Qy 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 249 ----- 248
Qy 481 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDSLRFEQSNNTARTYLRGNG 540
Db 249 ----- 248
Qy 541 SYNLYRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARF 586
Db 249 -----LSSIGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARF 287

RESULT 14

AAW31199

ID AAW31199 standard; Protein; 706 AA.

XX AAW31199;

DT 13-FEB-1998 (first entry)

XX *Bacillus popilliae* crystal protein.

DE Crystal protein; beetle; Scarabaeidae; maybug; cockchafer;

XX agricultural pest; spore; *Bacillus thuringiensis*; cytotoxic protein;

XX fusion protein; transgenic plant.

OS *Bacillus popilliae*.

XX Key Location/Qualifiers

FT Protein 1..706

FT /label= crystal protein

XX DE19642729-A1.

XX 24-APR-1997.

XX 17-OCT-1996; 96DE-1042729.

XX 18-OCT-1995; 95DE-1040223.

XX (UYHE-) UNIV HEIDELBERG.

XX Krieger L, Schnetter W, Zhang J;

XX WPI; 1997-237512/22.

XX N-PSDB; AAT89348.



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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:15:20 ; Search time 21 Seconds
(without alignments)
1273.355 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3043.5	91.8	634	4	US-09-186-002-12
2	3015.5	91.0	635	3	US-09-041-991A-4
3	3015.5	91.0	635	4	US-09-608-533A-4
4	3010.5	90.8	633	4	US-09-186-002-18
5	3005.5	90.7	634	4	US-09-186-002-2
6	2914.5	87.9	633	3	US-09-041-991A-10
7	2914.5	87.9	633	4	US-09-608-533A-10
8	2913.5	87.9	633	3	US-09-041-991A-8
9	2913.5	87.9	633	4	US-09-608-533A-8
10	2610.5	78.8	623	3	US-09-041-991A-6
11	2610.5	78.8	623	4	US-09-608-533A-6
12	1080	32.6	706	3	US-09-408-820-2
13	336.5	10.2	644	3	US-08-793-331-7
14	327.5	9.9	648	3	US-08-286-870A-4
15	327.5	9.9	719	3	US-08-286-870A-8
16	311.5	9.4	1156	4	US-09-002-285-72
17	311.5	9.4	1156	4	US-09-589-477-72
18	307	9.3	1157	2	US-08-532-547-5
19	307	9.3	1157	2	US-08-379-656B-5
20	307	9.3	1157	3	US-08-455-838-5
21	307	9.3	1157	3	US-09-019-809-5
22	307	9.3	1157	4	US-09-471-177-5
23	306	9.2	1138	1	US-07-973-320-2
24	306	9.2	1138	1	US-07-973-320-4
25	305.5	9.2	643	3	US-09-178-252-25
26	305.5	9.2	1186	3	US-09-178-252-23
27	305.5	9.2	1227	1	US-08-448-170-8

28	305.5	9.2	1227	3	US-08-961-803-9	Sequence 9, Appli
29	304.5	9.2	625	2	US-08-532-547-7	Sequence 7, Appli
30	304.5	9.2	625	2	US-08-532-547-9	Sequence 9, Appli
31	304.5	9.2	625	3	US-09-019-809-7	Sequence 7, Appli
32	304.5	9.2	625	3	US-09-019-809-9	Sequence 9, Appli
33	304.5	9.2	625	4	US-09-471-177-7	Sequence 7, Appli
34	304.5	9.2	625	4	US-09-471-177-9	Sequence 9, Appli
35	294.5	8.9	1176	1	US-08-434-823-2	Sequence 2, Appli
36	294.5	8.9	1176	1	US-08-457-366-2	Sequence 2, Appli
37	293.5	8.9	1229	1	US-08-100-709-4	Sequence 4, Appli
38	293.5	8.9	1229	1	US-08-176-865-4	Sequence 4, Appli
39	293.5	8.9	1229	1	US-08-474-038-4	Sequence 4, Appli
40	293.5	8.9	1229	2	US-08-779-046-4	Sequence 4, Appli
41	293.5	8.9	1229	2	US-08-881-340-4	Sequence 4, Appli
42	292	8.8	488	1	US-08-448-170-10	Sequence 10, Appli
43	292	8.8	488	3	US-08-961-803-10	Sequence 10, Appli
44	291.5	8.8	1179	1	US-08-040-751-1	Sequence 1, Appli
45	288.5	8.7	1176	1	US-07-828-788A-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-186-002-12
; Sequence 12, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-186-002-12

Query Match	91.8%;	Score 3043.5;	DB 4;	Length 634;
Best Local Similarity	90.7%;	Pred. No. 1.4e-262;		
Matches	573;	Conservative	34;	Mismatches 24; Indels 1; Gaps 1;
QY	2	NNVLNNGRTTICDAYNVVAHDPPSFEHKS	LDTIRKEWMEWKRTDHSLSYVAPIVGTVSSFL	61
Db	3	NNVLNNGRTTICDAYNVVAHDPPSFEHKS	LDTIQKEWMEWKRTDHSLSYVAPIVGTVSSFL	62
QY	62	LKKVGLIGKRIISELSELWGLIFP	SGSTNLMQDILRETEQFLNQLRNTDTLARVNAELEGLO	121
Db	63	LKKVGLIGKRIISELSELWGLIFP	SGSTNLMQDILRETEQFLNQLRNTDTLARVNAELEGLO	122
QY	122	ANIREFNQVDNLFNPTQNPVPLS	ITSSVNTMQQLFNRLPQFRVQGYQLLLPLFAQAA	181
Db	123	ANIREFNQVDNLFNPTQNPVPLS	ITSSVNTMQQLFNRLPQFIQGYQLLLPLFAQAA	182
QY	182	NMHLSFIRDVVLNADWEGISAAT	LRTYQNYLKNYTYEYSNYCINTYQTAFGLNTRLHDM	241
Db	183	NMHLSFIRDVVLNADWEGISAAT	LRTYRDYLRNYTRDYSNYCINTYQTAFGLNTRLHDM	242
QY	242	LEFRTYMFNLVFEYVSIWSLF	KYQSLVSSGANLYASGSGPQQTQSFTSQDPFFLYSLFQ	301
Db	243	LEFRTYMFNLVFEYVSIWSLF	KYQSLVSSGANLYASGSGPQQTQSFTSQDPFFLYSLFQ	302
QY	302	VNSNYVLNGFSGARLTQTFPN	IGLPGTTTHALLAARVNSYGGVSSGIGIGAV-FNQNFS	360
Db	303	VNSNYILSGISGTRLSITFPN	IGLPGSTTHLSNSARVNSYGGVSSGIGIGATNLNHNFN	362
QY	361	CSTFLPPLLTFFVRSWLDSG	SDRGVNTVTNMQTESFESTLGLRCGAFTARGNSNYFPDY	420

Db 363 CSTVLPLSTPFVRSWLDSTDRGCVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPDY 422
QY 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 423 FIRNISGVPLVVRNEDLRPLHYNQIRNIESPSGTPGGRAYLVSVHNRKNNIYAAENG 482
QY 481 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRPEQSNNTTARYTLRGNGN 540
Db 483 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRPEQSNNTTARYTLRGNGN 542
QY 541 SYNLYRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGVNVASDNT 600
Db 543 SYNLYRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNIVASDNT 602
QY 601 NVPLDINVTNFSGTQFELNMIMFVPTNLPPIY 632
Db 603 NVTLDINVTNLSGTPFDLMNIMFVPTNLPPLY 634

RESULT 2

US-09-041-991A-4
; Sequence 4, Application US/09041991A
; Patent No. 6107278
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-4

Query Match 91.0%; Score 3015.5; DB 3; Length 635;
Best Local Similarity 90.2%; Pred. No. 4.3e-260;
Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;
QY 1 MNVNLNGRTTICDAYNVVAHDPFSEHKSLDTIRKEWNEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNVNLNGRTTICNAYNVVAHDPFSEHKSLDTIQEENWNEWKRTDHSLYVAPVGTVSSF 60
QY 61 LLKKVGSGLIGKRLSELWGLIFPSGSGTNLMQDILRETEQFLNQLNTDTLARVNAELEG 120
Db 61 LLKKVGSGLIGKRLSELWGLIFPSGSGTNLMQDILRETEQFLNQLNTDTLDRVNAELEG 120

QY 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPOERVQGYQLLLPLFAQA 180
Db 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPOFQIQGYQLLLPLFAQA 180
QY 181 ANMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANMHLSFIRDVVLNADWEGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEFRTYMLNFVEYVSIWSLFKYQSLLVSSGANLYASGSPQQTQSFSDWPFYLSLF 300
Db 241 MLEFRTYMLNFVEYVSIWSLFKYQSLMVSSGANLYASGSPQQTQSFSAQNPFYLSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFPNIGGLPGTTTTTHALLAARVNYSGVSSGDIQAV-ENQNF 359
Db 301 QVNSNYILSGISGNRLSTTFPNIGGLPGSTTHSLNSARVNYSGVSSGGLIGATNLNHNH 360
QY 360 SCSTFLPPLLTPFVRSWLDSDRGGVNTVTNMQTESFESTLGLRCGA--FTARGNSNYF 417
Db 361 NCSTVLPLSTPFVRSWLDSDRGVATSTTWQTESFQITSLRCGAFPSARGNSNYF 420
QY 418 PDYFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVH 477
Db 421 PDYFIRNISGVPLVVRNEDLRPLHYNQIRNIESPSGTPGGLRAYMVSVHNRKNNIYAAH 480
QY 478 ENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTTARYTLRG 537
Db 481 ENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTTARYTLRG 540
QY 538 NGNSYNLYRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGVNVAS 597
Db 541 NGNSYNLYRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNVVAS 600
QY 598 DNTNVPLDINVTNFSGTQFELNMIMFVPTNLPPIY 632
Db 601 DNTNVPLDINGTSSGTQFELNMIMFVPTNLPPLY 635

RESULT 3

US-09-608-533A-4
; Sequence 4, Application US/09608533A
; Patent No. 6534644
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,533A
; FILING DATE: 30-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,991
; FILING DATE: 13-MARCH-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-608-533A-4

Query Match 91.0%; Score 3015.5; DB 4; Length 635;
Best Local Similarity 90.2%; Pred. No. 4.3e-260;
Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIQEEMWMEWKRTDHSLYVAPVGTVSSF 60

QY 61 LLKKVGSLLIGKRILSELWGLIPFSGSTNLMQDILRETEQFLNQLRNTDTTLARVNAELEG 120
Db 61 LLKKVGSLLIGKRILSELWGLIPFSGSTNLMQDILRETEQFLNQLRNTDTTLDRVNAELEG 120

QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVILNADEWGISAAATLRTYQNYLKNYTTSEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANMHLSFIRDVILNADEWGISAAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHD 240

QY 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTSQTSQDWPFYSLF 300
Db 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTSQTAQNWPFLYSLF 300

QY 301 QVNSNYVLNGFSGARLTQTFFNIGGLPGTTTHALLAARVNSYGGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYILSGISGNRLSTFFNIGGLPGSTTHLSNARVNSYGGVSSGLIGATNLNHNF 360

QY 360 SCSTFLPPLLTPEFVRSWLDGSDRGGVNTVNTWQTESFESTLGLRCGA--FTARGNSNYF 417
Db 361 NCSTVLPPLSTPEFVRSWLDGSDTREGVATSTTWQTESFQITSGLRCGAFPPSARGNSNYF 420

QY 418 PDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVH 477
Db 421 PDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYMVSVHNRKNNIYAAH 480

QY 478 ENGTMHILAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTARYTLRG 537
Db 481 ENGTMHILAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTARYTLRG 540

QY 538 NGNSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDIMGNVVAS 597
Db 541 NGNSYNLYLRVSSLSGNSTIRVTINGRVYTPVNVNTNNDGVNDGVIDNGARFSDINIGNVVAS 600

QY 598 DNTNVPDLINVTNSGTQFELMNMIFVPTNLPPIY 632
Db 601 DNTNVPDLINGTLSSGTQFELMNMIFVPTNLPPLY 635

RESULT 4
US-09-186-002-18
; Sequence 18, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-186-002-18

Query Match 90.8%; Score 3010.5; DB 4; Length 633;
Best Local Similarity 89.7%; Pred. No. 1.2e-259;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNSVLNNGRTTICDAYNVVAHDPFSEHKSLDTVQKEWTKNNHSLYLDPIVGTVASF 60

QY 61 LLKKVGSLLIGKRILSELWGLIFPSGSTNLMQDILRETEQFLNQLRNTDTTLARVNAELEG 120
Db 61 LLKKVGSLLIGKRILSELWGLIFPSGSTNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL 120

QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNLFNPNRNAVPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVILNADEWGISAAATLRTYQNYLKNYTTSEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANHLSFIRDVILNADEWGISAAATLRTYRDYLRNYTRDYSNYCINTYQSAFKGLNTRLHD 240

QY 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTSQTSQDWPFYSLF 300
Db 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTSQTSQDWPFYSLF 300

QY 301 QVNSNYVLNGFSGARLTQTFFNIGGLPGTTTHALLAARVNSYGGVSSGDIGA-VFNQNF 359
Db 301 QVNSNYVLNGFSGARLSNTFPNIVGLPGSTTHALLAARVNSYGGISSGDIGASPPNQNF 360

QY 360 SCSTFLPPLLTPEFVRSWLDGSDRGGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTFLPPLLTPEFVRSWLDGSDREGVATVNTWQTESFETTLGLRSGAFARGNSNYFPD 420

QY 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGRAYMVSVHNRKNNIHAVHEN 480

QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTARYTLRGNG 539
Db 481 GSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTARYTLRGNG 540

QY 540 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDIMGNVVASDN 599
Db 541 NSYNLYLRVSSLSGNSTIRVTINGRVYTATNVTNTTNDGVNDNGARFSDINIGNVVASN 600

QY 600 TNVPLDINVTNSGTQFELMNMIFVPTNLPPIY 632
Db 601 SDVPLDINVTNSGTQFELMNMILVPTNISPLY 633

RESULT 5
US-09-186-002-2
; Sequence 2, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

US-09-186-002-2

Query Match 90.7%; Score 3005.5; DB 4; Length 634;
Best Local Similarity 89.7%; Pred. No. 3.3e-259;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;
QY 2 NNVLNNGRTTICDAYNVVAHDPPSEFHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSFL 61
Db 3 NSVLNNGRTTICDAYNVVAHDPPSEFHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSFL 62
QY 62 LKKVGLIGKRIILSELWGLIFPPSGSTNLMQDILRETEQFLNRLPQFRVQGYQLLLPLFAQAA 121
Db 63 LKKVGLIGKRIILSELWGLIFPPSGSTNLMQDILRETEQFLNRLPQFRVQGYQLLLPLFAQAA 122
QY 122 ANIREFQVNDNFPNTPQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQAA 181
Db 123 ANVEEFNRQVNDNFPNTPNNAVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQAA 182
QY 182 NMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHDM 241
Db 183 NLHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHDM 242
QY 242 LEFRTYMFNLVFEYVSIWSLFLKQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLFQ 301
Db 243 LEFRTYMFNLVFEYVSIWSLFLKQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLFQ 302
QY 302 VNSNYVLNGFSGARLTQTFPNIIGLPGTTHALLAARVNYSGVSSGDIGA-VFNQNF 360
Db 303 VNSNYVLNGFSGARLTQTFPNIIGLPGTTHALLAARVNYSGVSSGDIGA-VFNQNF 362
QY 361 CSTFLPPLLTPFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPDY 420
Db 363 CSTFLPPLLTPFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPDY 422
QY 421 FIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 423 FIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 482
QY 481 TMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNGN 540
Db 483 TMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNGN 542
QY 541 SYNLVLRVSSLGNSSTIRVTINGRVTYASNVNTTNDGVNDNGARFLDINMGVNVASDNT 600
Db 543 SYNLVLRVSSLGNSSTIRVTINGRVTYASNVNTTNDGVNDNGARFLDINMGVNVASDNT 602
QY 601 NVPLDINVTNFGSGTQFELMNMVPTNLPIY 632
Db 603 DVPLDINVTNFGSGTQFELMNMVPTNLPIY 634

RESULT 6

US-09-041-991A-10
; Sequence 10, Application US/09041991A
; Patent No. 6107278
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,991A
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-991A-10

Query Match 87.9%; Score 2914.5; DB 3; Length 633;
Best Local Similarity 87.0%; Pred. No. 4.3e-251;
Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;

QY 1 MNVLNNGRTTICDAYNVVAHDPPSEFHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNVLNNGRTTICDAYNVVAHDPPSEFHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSF 60
QY 61 LLKKVGLIGKRIILSELWGLIFPPSGSTNLMQDILRETEQFLNRLPQFRVQGYQLLLPLFAQA 120
Db 61 LLKKVGLIGKRIILSELWGLIFPPSGSTNLMQDILRETEQFLNRLPQFRVQGYQLLLPLFAQA 120
QY 121 QANIREFQVNDNFPNTPQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVNDNFPNTPNNAVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
QY 181 ANMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANIHLSYIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEFRTYMFNLVFEYVSIWSLFLKQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWSLFLKQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFPNIIGLPGTTHALLAARVNYSGVSSGDI-GAVFNQNF 359
Db 301 QVNSNYVLNGFSGARLTQTFPNIIGLPGTTHALLAARVNYSGVSSGDI-GAVFNQNF 360
QY 360 SCSTFLPPLLTPFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCNTISPPLSTSFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYYPG 420
QY 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 480
QY 480 GTMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 540
QY 540 NSYNLYLRVSSLGNSSTIRVTINGRVTYASNVNTTNDGVNDNGARFLDINMGVNVASDN 599
Db 541 NSYNLYLRVSSLGNSSTIRVTINGRVTYASNVNTTNDGVNDNGARFLDINMGVNVASDN 600
QY 600 TNVPLDINVTNFGSGTQFELMNMVPTNLPIY 632
Db 601 SDVPLDINVTNFGSGTQFELMNMVPTNLPIY 633

RESULT 7

US-09-608-533A-10
; Sequence 10, Application US/09608533A
; Patent No. 6534644

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Narva, Kenneth E.
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/608,533A
FILING DATE: 30-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,991
FILING DATE: 13-MARCH-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-608-533A-10
Query Match 87.9%; Score 2914.5; DB 4; Length 633;
Best Local Similarity 87.0%; Pred. No. 4.3e-251;
Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;
QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNNVLNNGRTTICDAYNVVVDHPFSEHKSLDTIQKEWMEWKDNHSLYVDPIVGTVASF 60
QY 61 LLKKVGSLLIGKRILSELWGLIFPPSGSTNLMQDILRETEQFLNQLNTDTLARVNAELEG 120
Db 61 LLKKLGSLLIGKRILSELRLNLIFFPSGSTNLMEDILRETEKFLNKLNTDTLSRVNAELTGL 120
QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNLFNPNRNAVPLSITSSVNTMQQLFLNRLSQFQMKGYYQLLLPLFAQA 180
QY 181 ANMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTTSEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANIHLSYIRDVILNAAEEWGISAAATLRTYQNHLNRYTRDYSNYCIDTYQTAFRGLNTRIHD 240
QY 241 MLEFRTYMFNLNVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTSQTSQDWPFYSLF 300
Db 241 MLEFRTYMFNLNVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTLFTSQDWPFYSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFPNIGLPGTTTHALLAARVNSYSGVSSGDI-GAVENQNF 359
Db 301 QVNSNYVLGFSGASLFTTFPNIGLPGSTTTQALLAARVNSYSGGITSIGSISGNSFNQNF 360
QY 360 SCSTFLPPLLTFFVRSWLDGSDRGGVNTVTNWQTESFESTGLRCGAFTARGNSNYFPD 419
Db 361 NCNTISPPLSTSFVRSWLDGSDRQGVTTVTNWQTESFETTSGLRCGAFTPRGNSNYYPG 420

QY 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYIYAVHEN 479
Db 421 YFIRNISGVSLVRNEDLKRPLYNEKRNIESPSGTPGGARAYMVSVHNRKNYIYAVHEN 480
QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNQDGLRFEQSNNTTARYTLRGNG 539
Db 481 GTMIHLAPEDNTGFTISPIHATQVNNQTRFISEKFGNQDGLRFEQSNNTTARYTLRGNG 540
QY 540 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGVNVVASN 599
Db 541 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNVVASSN 600
QY 600 TNVPLDINVTFNSGTQFELMNMIFVPTNLPPIY 632
Db 601 SDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY 633
RESULT 8
US-09-041-991A-8
Sequence 8, Application US/09041991A
Patent No. 6107278
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-8

Query Match 87.9%; Score 2913.5; DB 3; Length 633;
Best Local Similarity 87.2%; Pred. No. 5.3e-251;
Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;
QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNNVLNNGRTTICDAYNVVVDHPFSEHKSLDTIQKEWMEWKDNHSLYVDPIVGTVASF 60
QY 61 LLKKVGSLLIGKRILSELWGLIFPPSGSTNLMQDILRETEQFLNQLNTDTLARVNAELEG 120
Db 61 LLKKLGSLLIGKRILSELRLNLIFFPSGSTNLMEDILRETEKFLNKLNTDTLSRVNAELTGL 120
QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180

Db 121 QANVEEFNRQVDNFLNPNRNVAPLSITSSVNTMQQLFNLRLSQFQMGYQQLLLPLFAQA 180
QY 181 ANMHLSPFIRDVVLNADENGISAATLRTYQNLKNTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANLHLSFIRDVILNAEENGISAATLRTYQNLKNTTEYSNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEPRTYMFNLVFEYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEPRTYMFNLVFEYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFNIGGLPGTTTTHALLAARVNYSGVSSGDI-GAVFNQNF 359
Db 301 QVNSNYVLNGFSGASLTFTFENIGGLPGTTTTHALLAARVNYSGGITSGSGSNFYPG 360
QY 360 SCSTFLPPLLTFFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCNTISPPPLSTSFVRIWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYYPG 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVSLVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 480
QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 539
Db 481 GTMIHLAPEDNTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 540
QY 540 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDINMGVNVASDN 599
Db 541 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNVNVASSN 600
QY 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPIY 632
Db 601 SDVPLDINVTLSGTQFELNMIMLVPTNLPLY 633

RESULT 9

US-09-608-533A-8
; Sequence 8, Application US/09608533A
; Patent No. 6534644
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; Narva, Kenneth E.
; Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,533A
; FILING DATE: 30-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,991
; FILING DATE: 13-MARCH-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-608-533A-8

Query Match 87.9%; Score 2913.5; DB 4; Length 633;
Best Local Similarity 87.2%; Pred. No. 5.3e-251;
Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;

QY 1 MNVNLNNGRTTICDAYNVVAHDPPFSFEHKSLLDTIRKEWMEWKRTDHSLSYVAPIVGTVSSF 60
Db 1 MNVNLNNGRTTICDAYNVVAHDPPFSFEHKSLLDTIRKEWMEWKRTDHSLSYVAPIVGTVSSF 60
QY 61 LLKKVGSLLIGKRIILSELWGLIFPSGGSNTLMODILRETEQFLNQLNLTDTLARVNAELEG 120
Db 61 LLKKVGSLLIGKRIILSELWGLIFPSGGSNTLMODILRETEQFLNQLNLTDTLARVNAELEG 120
QY 121 QANIREFNQVDNPLNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNPLNPNRNVAPLSITSSVNTMQQLFNLRLSQFQMGYQQLLLPLFAQA 180
QY 181 ANMHLSPFIRDVVLNADENGISAATLRTYQNLKNTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANLHLSFIRDVILNAEENGISAATLRTYQNLKNTTEYSNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEPRTYMFNLVFEYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEPRTYMFNLVFEYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFNIGGLPGTTTTHALLAARVNYSGVSSGDI-GAVFNQNF 359
Db 301 QVNSNYVLNGFSGASLTFTFENIGGLPGTTTTHALLAARVNYSGGITSGSGSNFYPG 360
QY 360 SCSTFLPPLLTFFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCNTISPPPLSTSFVRIWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYYPG 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVSLVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 480
QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 539
Db 481 GTMIHLAPEDNTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNG 540
QY 540 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDINMGVNVASDN 599
Db 541 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNVNVASSN 600
QY 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPIY 632
Db 601 SDVPLDINVTLSGTQFELNMIMLVPTNLPLY 633

RESULT 10

US-09-041-991A-6
; Sequence 6, Application US/09041991A
; Patent No. 6107278
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida

```

; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,991A
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-041-991A-6

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	Query Match	78.8%;	Score 2610.5;	DB 3;	Length 623;
	Best Local Similarity	80.3%;	Pred. No. 5.2e-224;		
	Matches 508;	Conservative 46;	Mismatches 68;	Indels 11;	Gaps 6;
QY	1	MNVNLNNGRTTICDAYNVVAHDPFSFEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSF	60		
DB	1	MNVNLNNGRTTICDAYNVVAHDPFSFEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSF	60		
QY	61	LLKKVGLIGKRILSELWGLIFPPSGSTNLMQDILRETEQFLNQLRINTDTLARVNAEGL	120		
DB	61	LLKKVGLIGKRILSELWGLIFPPSGSTNLMQDILRETEQFLNQLRINTDTLARVNAEGL	120		
QY	121	QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA	180		
DB	121	QANVAEFNRQVDNLFNPNQNPVPLAIDSVNTLQQLFLSRLPQFQIQGYQLLLPLFAQA	180		
QY	181	ANMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTTESYNYCINTYQTAERGLNTRLHD	240		
DB	181	ANLHLSFIRDVILNADEWGISAAATVTRYRDHLRNFTRDYSNYCINTYQTAERGLNTRLHD	240		
QY	241	MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF	300		
DB	241	MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGP--TQSFTAHPWFLYSLF	298		
QY	301	QVNSNYVLNGFSGARLTQTFEPNIGGLPGTTTTHALLAARVNYSGVSSGDIG-AVFNQNF	359		
DB	299	QVNSNYVLNGLSGARTTTFISNIGGLPGSTTTQTLHFARINRGGVSSSRIGQANLNQNF	358		
QY	360	SCSTFLPPLLTPEVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNVPFD	419		
DB	359	NISTLFNPLQTPFIRSWLDGSDTDREGVATSTNWQSGAFETTL-LRFSIFSARGNSNFPFD	417		
QY	420	YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN	479		
DB	418	YFIRNISGVVGTISNADLARPLHFNEIRDI---GTTA--VASLTVHNRKNNIYDTHEN	471		
QY	480	GTMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNG	539		
DB	472	GTMIHLAPNDYTGTVSPIHATQVNNQIRTFISEKYGNQGDSLRFELSNTTARYTLRGNG	531		
QY	540	NSYNLYLRVSSLGNSTTRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDN	599		
DB	532	NSYNLYLRVSSIGSSTIRVTINGRVYTA-NVNTTTNNDGVLDNGARFSDINIGNVVASAN	590		
QY	600	TNVPLDINVTFSNGTQFELNMIMFVPTNLPIY	632		

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Db      591  TNVPLDIQVTFNGNPQFELMNMIMFVPTNPSPLY  623

RESULT 11
US-09-608-533A-6
; Sequence 6, Application US/09608533A
; Patent No. 6534644
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
;           Narva, Kenneth E.
;           Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,533A
; FILING DATE: 30-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,991
; FILING DATE: 13-MARCH-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-608-533A-6

Query Match      78.8%; Score 2610.5; DB 4; Le
Best Local Similarity 80.3%; Pred. No. 5.2e-224;
Matches 508; Conservative 46; Mismatches 68; In

QY      1  MNVVLNNGRTTICDAYNVVAHDPFSFEHKSLSLDTIRKEWMKWR
Db      1  MNVVLNSGRNTTCHAHNVVAHDPFSFEHKSLSLNTIEKWKWKWR
QY      61  LLKKGSLIGKRILSELWGLIFPSGSTNLMDILRETEQFLNQ
Db      61  LLKKGSLVGKRILSELQNLIFPSGSIDLMDQILRATEQFINQ
QY      121 QANIREFNQQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQ
Db      121 QANVAEFNRQVDNFLNPNQNPVPLAIDSVNTLQQLFLSRLPQ
QY      181 ANMHLSFIRDVVLNADWGISAAATLRTYQNLKYNVTTEYSNYC
Db      181 ANLHLSFIRDVILNADWGISAAATVTRYDHLRNFTRDYSNYC
QY      241 MLEFRTYMFLNVFEYVSIWSLFKYQSLVSSCANLYASGSGPQ
Db      241 MLEFRTYMFLNVFEYVSIWSLFKYQSLVSSCANLYASGSGP-

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QY 301 QVNSNYVLNGFSGARLTQTFFNIGGLPGTTTHALLAARVNSGGVSSGDIG-AVENQNF 359
DDB 299 QVNSNYVLNGLSGARTTITFENIGGLPGTTTQTLHFARINRGVSSSRIGQANLQNF 358
QY 360 SCSTFLPPLLTFFVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPD 419
DDB 359 NISTLFNPLQTPFIRSWLDSGTDREGVATSTNWQSGAFETTL-LRFSIFSARGNSNFFPD 417
QY 420 YFIRNISGVPLVVRNEDLRPLHNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
DDB 418 YFIRNISGVVGTISNADLARPLHNEIRDI----GTGA--VASLVTVHNRKNNIYDTHEN 471
QY 480 GTMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNG 539
DDB 472 GTMIHLAPNDYTGTVSPHATQVNNQIRTFISEKYGNQGDSLRFELSNTTARYTLRGNG 531
QY 540 NSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTNNDGVNDNGARFLDINMGVNVASDN 599
DDB 532 NSYNLYLRVSSIGSSTIRVTINGRVYTA-NVNTTNNNDGVLDNGARFSDINIGNVVASAN 590
QY 600 TNVPLDINVTENSQTQFELNMIMFVPTNLPIY 632
DDB 591 TNVPLDIQVTFNGNPQFELNMIMFVPTNPSPLY 623

RESULT 12
US-09-408-820-2
; Sequence 2, Application US/09408820
; Patent No. 6204057
; GENERAL INFORMATION:
; APPLICANT: Schmetter, Wolfgang
; APPLICANT: Krieger, Lutz
; APPLICANT: Zhang, Jianning
; TITLE OF INVENTION: Polynucleotides And The Proteins Encoded Thereby,
; TITLE OF INVENTION: Suitable For Controlling Lamellicorn Beetles
; FILE REFERENCE: S-30403/A/UHD/CGC1996/PCT
; CURRENT APPLICATION NUMBER: US/09/408,820
; CURRENT FILING DATE: 1999-09-29
; EARLIER APPLICATION NUMBER: 09/051,454
; EARLIER FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: DE 195 40 223.5
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Bacillus popilliae
; FEATURE:
; OTHER INFORMATION: strain subspecies: melolonthae H1; stage of
; OTHER INFORMATION: development: spore stage; cell type: sporangium
; FEATURE:
; OTHER INFORMATION: immediate origin: isolate from the haemolymph of
; OTHER INFORMATION: Melolontha melolontha individuals captured on open
; OTHER INFORMATION: ground
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(706)
; OTHER INFORMATION: mature protein crystal peptide determined by
; OTHER INFORMATION: experiment
US-09-408-820-2

Query Match 32.6%; Score 1080; DB 3; Length 706;
Best Local Similarity 38.4%; Pred. No. 1.7e-87;
Matches 264; Conservative 96; Mismatches 233; Indels 94; Gaps 21;
QY 2 NNVLNN-----GRTTICDA---YNNVAHDPFSEHKSLDTIRKEWMEWKRTD 45
DDB 58 NNDNNDAICDELGLTPIDNNNTICSTFTPINVMRTDP--FRKSTQELTRETWEWKENS 115
QY 46 HSLYVAPIGVTVSSFLKKVGLSLIGKRIKILSELWGLFPSPGSTNLMDILRETEQFLNQL 105
DDB 116 PQLFTPAIVGVVTSFLQSLKKQATSFLLKTLTDLFPNNSSLTMEELIRATEQYVQERL 175

QY 106 NTDTLARVNAELEGQLQANIREFNQOVDFNFTQNPVPLSITSSVNTMQQLFNLRLPQFR 165
DDB 176 DTDYANRVSQELVGLKNNLTTFNDQVEFQNRVIGISPLAIDSINTMQQLFVNRLPQFQ 235
QY 166 VQGYQLLLPLFAQAANMHLFSIRDVVLNADWGISAAATLRTYQNLKNTTETYSNYCIN 225
DDB 236 VSGYQVLLPLFAQAATLHLTFLRDVIINADENIPTAQLNTYTRYFYKEYIAEYSNYALS 295
QY 226 TYQTAFRGLNTR-----LHDMLEFRTYMFELNVFEYVSIWSLFKYQSLVSSGANLYASG 279
DDB 296 TYDDGFR---TRFYPRNTLEDMLQKFTMTNALDLVSIWSLLKYVNLVSTSANLYNIG 352
QY 280 SGPQQTQSFTSQDWPFYLSLFQVNSNYVLNGFSGARLTQTFFNIGG-----LPGTTTTH 333
DDB 353 DNKVNAGYPISYGFFNFNSYIQTKSNYVLSGVSGIGARFTYSTVLGRYLHDDLKNIIT- 411
QY 334 ALLAARVNSGGVSSGDIGAVFN-----QNFSCTFLP-PLLTTP 371
DDB 412 -----YVGGTQGNIGVQLSTTTELDELKQQQATRDSLVDFFFTLNCMLPNPITAP 463
QY 372 -FVRSWLDSG-SDRGVNTVTNWQTESFESTLGL-RCGAFARGNSNYFPDYFIRNISGV 428
DDB 464 YFATSLYESRYSSIGYLRKDVFKSE--DSTCGLGNPGAWTS-----YPDYITNISAT 515
QY 429 PLVVRNEDLRPLHNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENGTMHIAPE 488
DDB 516 VOINGENTDTTPLYFKENRPITSTRGV-----NKVIAVYNRKANIAGTNQNGTMHQAAPP 570
QY 489 DYTGTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNG-NSYNLYLR 547
DDB 571 DGTGFTVSPLHPSA--NTITSYIKENYGNSGDSLHL-KGQGYLHMLSGNQDRYRLVLR 627
QY 548 VSSLGNSTIRVTINGRVYTASNVTNTNNDGVNDNGARFLDINMGVNVASDNVPLD 605
DDB 628 LSGAAN---QIKLQSPSTSIYAFDTSTNNEGTDNGSKFKDFAFSTPFVPEQK-----E 679
QY 606 INVTFNSGTQFELNMIMFVPTNLPIY 632
DDB 680 IVLYFEGVGSLLDMLNLIPLPADDTPLY 706

RESULT 13
US-08-793-331-7
; Sequence 7, Application US/08793331
; Patent No. 6071877
; GENERAL INFORMATION:
; APPLICANT: DELECLUSE, ARNELLE
; APPLICANT: THIERY, ISABELLE
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING A TOXIC ACTIVITY AGAINST
; TITLE OF INVENTION: INSECTS OF THE DIPTERA FAMILY
; FILE REFERENCE: 0660-0116-0 PCT
; CURRENT APPLICATION NUMBER: US/08/793,331
; CURRENT FILING DATE: 1997-05-13
; EARLIER APPLICATION NUMBER: PCT/FR95/01116
; EARLIER FILING DATE: 1995-08-24
; EARLIER APPLICATION NUMBER: FR 94/10299
; EARLIER FILING DATE: 1994-08-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 644
; TYPE: PRT
; ORGANISM: B. thuringiensis ser. israelensis
US-08-793-331-7

Query Match 10.2%; Score 336.5; DB 3; Length 644;
Best Local Similarity 23.1%; Pred. No. 2.7e-21;
Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;
QY 27 EHKSLDTIRKEWMEWKRTDHSLY-----VAP---IVGTVSSFLKKVGLSLIGKRIKIL 76
DDB 3 EDSSDLTSLIV---NETDFLYNNYTEPTIAPALIAVAPIAQYLAATAIGKWAFAAFSK 58

Db 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596

Qy 587 LDINMGNVASDNTNVPDLINVT-----FNSGTQFELMNMIFVPTNL 628

Db 597 LDYKTFRTVGTTPFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEV 645

RESULT 15

US-08-286-870A-8

Sequence 8, Application US/08286870A

Patent No. 6063605

GENERAL INFORMATION:

APPLICANT: ELY, S

APPLICANT: TAILOR, RH

APPLICANT: TIPPETT, JM

APPLICANT: BLENK, RG

TITLE OF INVENTION: BACTERIAL GENES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DABY & CUSHMAN

ADDRESSEE: Intellectual Property Group of

ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,870A

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/520228

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8910624.9

FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:

NAME: PAUL N. KOKULIS

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 70608/220720

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 719 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-286-870A-8

Query Match 9.9%; Score 327.5; DB 3; Length 719;

Best Local Similarity 22.8%; Pred. No. 2e-20;

Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;

Qy 21 HDPFSFEHK-----SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52

Db 9 HQSPSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFVSASTIQTGIGIAG 68

Qy 53 -IVGTVSSFLKKVGLIKRILSELWGLIFPSGSTNLMDILRETEQFLNQLNRTDILA 111

Db 69 KILGTGLGVFPFAGQVASLY-SFILGELW----PKGK-NQWEIFMEHVEEIIINQKISTYARN 122

Qy 112 RVNAELEGLOANIREFNQVDNPLNPTQNPVPLSIT-SSVNTMQQLFLNRLPQFRVQGYQ 170

Db 123 KALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPAVSGEE 182

Qy 171 LLLLPLFAQAANMHLSFIRDVVLNADWGISAATLRTYQNLKNTTYTEYSNYCINTYQTA 230

Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTG 242

Qy 231 FRGL-NTRLHMDL---EFRTYMLNVFEYVSIWSLFKYQSLLVSSGANL-----YASGSGP 282

Db 243 LNNLRGTNAESWVRYNQFRDRDMLMVLDLVALFPSYDTQMPYPIKTTAQLTREYTDAGT 302

Qy 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313

Db 303 VHPHSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGG 362

Qy 314 ARLTQTFPNIGGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQFSCSTFLPPLLPFV 373

Db 363 HKL-EFRTIGTGLNIST-----QGSTNTSINPVTLPFT 394

Qy 374 RSWLDSGSDRGGVNTVT-----NWQ--TESFESTLGLRCGAFTARGNSNYFPD 419

Db 395 SRDYYRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIAS-----DNFYYPG 441

Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYIYA-VHE 478

Db 442 Y-----AGIGTQLQDSNELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494

Qy 479 NGTMIHLAPEDYTGTTSPIHATQV-----NNQTRTFISEKFG-NQGDLSLRFQSNNTTA 531

Db 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNTGT 543

Qy 532 RYTLRGNGN-----SYNLYLRVSSSLGNSTIRVTINGRVYTASNWNTTNNNDGVNDNGARF 586

Db 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596

Qy 587 LDINMGNVASDNTNVPDLINVT-----FNSGTQFELMNMIFVPTNL 628

Db 597 LDYKTFRTVGTTPFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEV 645

Search completed: December 12, 2003, 16:18:44

Job time : 23 secs

Db 181 ANMHSFIRDVILNADEWGISAATLRTYRDYLRNTRDYSNYCINTYQTAFRLNTRLHD 240
Qy 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWSLFKYQGLMVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNYSGGVSSGGDIGAV-FNQNF 359
Db 301 QVNSNYILSGISGTRLSITFFPNIGGLPGSTTTTHSLNSARVNYSGGVSSGLIGATNLNHNH 360
Qy 360 SCSTFLPPLLTTPFVRSWLDGSDRGGVNTVTNWQTESPESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTVLPPLSTPFVRSWLDGSDTREGVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNQIRNIESPSGTPGGLRAYLVSVHNRKNNIYAAEN 480
Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLSNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDMGNVVASDN 599
Db 541 NSYNLYLRVSSLSNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDMGNVVASDN 600
Qy 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPPY 632
Db 601 TNVTLDINVTLSNGTFFDLNMIMFVPTNLPPLY 633

RESULT 2

Q9S6N5 PRELIMINARY; PRT; 633 AA.
ID Q9S6N5
AC Q9S6N5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cry2Aa protein.
GN CRY2AA6.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YZ71;
RA Yu J., Pang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene
RT cry2Aa6 from new isolated strain of Bacillus thuringiensis YZ71.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132465; CAA10672.1; -
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 633 AA; 70837 MW; CC727E333B75A583 CRC64;

Query Match 91.4%; Score 3029.5; DB 2; Length 633;
Best Local Similarity 90.0%; Pred. NO. 1.1e-195;
Matches 570; Conservative 36; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKSILDTIRKEWMEWKRTDHSLYVAPIVGTSSSF 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKSILDTIRKEWMEWKRTDHSLYVAPIVGTSSSF 60
Qy 61 LLKKVGSLLIGKRILSELWGLIFPSSGNTLMQDILRETEQFLNQLNTDTTLARVNAELEG 120
Db 61 LLKKVGSLLIGKRILSELWGLIFPSSGNTLMQDILRETEQFLNQLNTDTTLARVNAELEG 120
Qy 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNQQVDNLFNPTQNPAPLSITSSVNTMQQLFLNRLPQFIQGYQLLLPLFAQA 180

Qy 181 ANMHSFIRDVILNADEWGISAATLRTYQNYLKNTTEYSNYCINTYQTAFRLNTRLHD 240
Db 181 ANMHSFIRDVILNADEWGISAATLRTYRDYLRNTRDYSNYCINTYQTAFRLNTRLHD 240
Qy 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLMVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNYSGGVSSGGDIGAV-FNQNF 359
Db 301 QVNSNYILSGISGTRLSITFFPNIGGLPGSTTTTHSLNSARVNYSGGVSSGLIGATNLNHNH 360
Qy 360 SCSTFLPPLLTTPFVRSWLDGSDRGGVNTVTNWQTESPESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTVLPPLSTPFVRSWLDGSDTREGVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNQIRNIESPSGTPGGLRAYLVSVHNRKNNIYAAEN 480
Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLSNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDMGNVVASDN 599
Db 541 NSYNLYLRVSSLSNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFELDMGNVVASDN 600
Qy 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPPY 632
Db 601 TNVTLDINVTLSNGTFFDLNMIMFVPTNLPPLY 633

RESULT 3

Q9S6N4 PRELIMINARY; PRT; 633 AA.
ID Q9S6N4
AC Q9S6N4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cry2Aa protein.
GN CRY2AA5.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL39;
RA Yu J., Pang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene
RT cry2Aa5 from new isolated strain of Bacillus thuringiensis SL39.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132464; CAA10671.1; -
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 633 AA; 70925 MW; 8FB7F5216AC6F7B8 CRC64;

Query Match 91.3%; Score 3025.5; DB 2; Length 633;
Best Local Similarity 90.0%; Pred. No. 2e-195;
Matches 570; Conservative 35; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKSILDTIRKEWMEWKRTDHSLYVAPIVGTSSSF 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPPFSFEHKSILDTIRKEWMEWKRTDHSLYVAPIVGTSSSF 60
Qy 61 LLKKVGSLLIGKRILSELWGLIFPSSGNTLMQDILRETEQFLNQLNTDTTLARVNAELEG 120
Db 61 LLKKVGSLLIGKRILSELWGLIFPSSGNTLMQDILRETEQFLNQLNTDTTLARVNAELEG 120
Qy 121 QANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180

Db 121 QANIREFNQVDNFLNFTQNPVPLSITSSVNTMQQLFNRLPQFQIQGYQLLLPLFAQA 180
Qy 181 ANMHLSFIRDVVLNADGWGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANMHLSFIRDVVLNADGWGISAATLRTYRDYLRNTRDYSNYCINTYQTAFRGLNTRLHD 240
Qy 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLLVSSGANLYASGGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLMVSSGANLYASGGPQQTQSFTAQWPFYSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTTPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYILSGISGRLSITFPNIGGLPGSTTTTHLSNARVNYSGGVSSGLICATNLNHNF 360
Qy 360 SCSTFLPPLLTPFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTVLPLSTPFVRSWLDGSDTREGVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGARAYLVSVHNRKNNIYAANEN 480
Qy 480 GTMIHLAPEDYTGTFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGTFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTARHTLRGNG 540
Qy 540 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDN 599
Db 541 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNIVASDN 600
Qy 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPIY 632
Db 601 TNVTLDINVTLSGTPFDLMNIMFVPTNLPLY 633

RESULT 4
Q8GH90 PRELIMINARY; PRT; 633 AA.
AC Q8GH90;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Crystal delta-endotoxin.
GN CRY2AB.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-Pr-88;
RA Li C., Zhang J., Huang D., Li G.;
RT "A crystal endotoxin from Bacillus thuringiensis strain B-Pr-88."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336115; AAO13296.1; -.
SQ SEQUENCE 633 AA; 70726 MW; 01EFA93A35564D01 CRC64;

Query Match 90.5%; Score 2998.5; DB 2; Length 633;
Best Local Similarity 89.4%; Pred. No. 1.3e-193;
Matches 566; Conservative 40; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTSSSF 60
Db 1 MNSVLNNGRTTICDAYNVVAHDPPSFQHKSLDTPVQKEWTEWKNHSLYLDPIVGTVASF 60
Qy 61 LLKKVGSGLIGKRIILSELWGLIFPPSGSTNLMQDILRETEQFLNQLNTDTLARVNAELEG 120
Db 61 LLKKVGSGLVGRILSELNLIFFPSGSTNLMQDILRETEKFLNQLNTDTVARVNAELTGL 120
Qy 121 QANIREFNQVDNFLNFTQNPVPLSITSSVNTMQQLFNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNFLNPNRNVPLSITSSVNTMQQLFNRLPQFQMCGYQLLLPLFAQA 180
Qy 181 ANMHLSFIRDVVLNADGWGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240

Db 181 ANHLSFIRDVILNADGWGISAATLRTYRDYLRNTRDYSNYCINTYQSAFKGLNTRLHD 240
Qy 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLLVSSGANLYASGGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLNFEYVSIWSLFKYQSLLVSSGANLYASGGPQQTQSFTSQDWPFLYSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTTPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGA-VFNQNF 359
Db 301 QVNSNYVLNGFSGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGGISGDIASPFNQNF 360
Qy 360 SCSTFLPPLLTPFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTFLPPLLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGISNYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHAVHEN 480
Qy 480 GTMIHLAPEDYTGTFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTARYTLRGNG 539
Db 481 GSMIHLAPNDYTGTFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDN 599
Db 541 NSYNLYLRVSSLSGNSTIRVTINGRVYTATNVNTTNTNDGVNDNGARFSDINIGNVVASN 600
Qy 600 TNVPLDINVTNSGTQFELNMIMFVPTNLPIY 632
Db 601 SDVPLDINVTLSGTPFDLMNIMLVPTNISPLY 633

RESULT 5

Q9RM89 PRELIMINARY; PRT; 551 AA.
AC Q9RM89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cry2A protein (Fragment).
GN CRY2AD.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cy29;
RA Yu J., Pang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene cry2Ad from new isolated strain of Bacillus thuringiensis CY29."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132463; CAA10670.2; -.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03945; endotoxin_N; 1.
FT NON TER 551 551
SQ SEQUENCE 551 AA; 62126 MW; D6B77B8AE713E98A CRC64;

Query Match 79.7%; Score 2641.5; DB 2; Length 551;
Best Local Similarity 90.4%; Pred. No. 1.2e-169;
Matches 498; Conservative 30; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTSSSF 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTIQKEWMEWKRTDHSLYVAPVGTSSSF 60
Qy 61 LLKKVGSGLIGKRIILSELWGLIFPPSGSTNLMQDILRETEQFLNQLNTDTLARVNAELEG 120
Db 61 LLKKVGSGLIGKRIILSELWGIIFFPSSTNLMQDILRETEQFLNQLNTDTLARVNAELIGL 120
Qy 121 QANIREFNQVDNFLNFTQNPVPLSITSSVNTMQQLFNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNQVDNFLNFTQNPVPLSITSSVNTMQQLFNRLPQFQIQGYQLLLPLFAQA 180

QY 181 ANMHLSPFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANMHLSPFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEFRTYMFNLVFEYVSIWLSFKYQSLVSSGANLYASGGPQQTSQFTSODWPFLYSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWLSFKYQSLVSSGANLYASGGPQQTSQFTSODWPFLYSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFFNIGGLPGTTTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYILSGISGTRLSITFFNIGGLPGSTTTHSLNARVNYSGVSSGLIGATNLNHF 360
QY 360 SCSTFLPPLLTFFVRSWLDSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTVLPPLSTFFVRSWLDSDRGVATSTNWQTESFQTTLSLRCGAFARGNSNYFPD 420
QY 420 YFIRNISGVPLVRNEDLRPLHYNIEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVRNEDLRPLHYNQIRNIESPSGTPGGLRAYLVSVHNRKNNIYAANEN 480
QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQSNNTTARVTLRGNG 539
Db 481 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQSNNTTARVTLRGNG 540
QY 540 NSYNLYLRVSS 550
Db 541 NSYNLYLRVSS 551

RESULT 6
Q8KNY2 PRELIMINARY; PRT; 1231 AA.
AC Q8KNY2;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CryIBII.
GN CRYIBII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=834;
RA Isakova I.A., Isakov Y.B., Rymar' S.E., Yarovoi S.V.;
RT "Cloning of a novel Bacillus thuringiensis cryIBII gene for
RT insecticidal crystal protein."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY138457; AAM93496.1; -
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 1231 AA; 139765 MW; C9F2848A9297EA00 CRC64;

Query Match 9.9%; Score 328.5; DB 2; Length 1231;
Best Local Similarity 23.3%; Pred. No. 2.1e-13;
Matches 155; Conservative 101; Mismatches 249; Indels 161; Gaps 29;
QY 52 PIVGTVSSFLKKVGSLLIGKRISELWGLIFPSGSTNLMDILRETEQFLNQLNTDTLA 111
Db 73 PFAGOLASFYSFLVG-----ELW---PSG-RDPWEIFLEHVEQLIRQQVTENTRN 118
QY 112 RVNAELEGQANIREFNQVDFNPTQNPVPLITSSVNTMQQL-FLNRLPQFRVQGYQ 170
Db 119 TAIARLEGLGRGYSYQQALETWLDNRNDARSIIERYVALELDITTAIFLIRNEE 178
QY 171 LLLLPLFAQAAMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTA 230
Db 179 VPLLMVYAQAANLHLLLRDASLFGSEWGMASSDVNQYQEQIRYTEYSNHCQWYNTG 238

QY 231 FRGL-NTRLHML--EFRTYMFNLVFEYVSIWLSFKYQSLVSSGANL-----YASGSGP 282
Db 239 LNNLRGTNAESWLRNQFRRLDTLGLVLDLVALFPSTYDTRTPINTSAQLTREIYTDPIGR 298
QY 283 QQTQS-FTSQDW-----PFLYSLFQVNSNYV-----LNGPSG 313
Db 299 TNAPSGFASTWNNNAPSFAIEAAIFRPHLLDFPEQLTIYSASSRWSSTQHMNYWVG 358
QY 314 ARLTQTFPNIGGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLTPPV 373
Db 359 HRL--NFRPIGGTLNTST-----QGLTNTSINPVTLOFT 391
QY 374 RSWLDSDSGDRGVN---TVTN---WQTESFESTLGLRCGAFARGNSNYFPDYFIRNIS 426
Db 392 SRDVTYRTESNAGTNILFTTPVNGVPWDRFNINPQNI-----YERGATTYSQPY----Q 441
QY 427 GVPLVVRNEDLRPLHYNIEIRNIESPS-----GTPGG--LRAYMVS-VH----- 467
Db 442 GVGQLFDSETELPETTERPNYESYSHRLSHIGLIIGNTLRAPVYSWTHRSADRTNTIG 501
QY 468 -NRKNNIYAVHE---NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSL 522
Db 502 PNRITQIPAVKGRFLFNGSVI--SGPGFTGDDVRLNRNNGNIQNRGYI-----EV 550
QY 523 RFEQSNNTTARYTLRGNGSNLYLRVSSLCNISTIRVTI-NGRVYTASNVTNTNNDGVND 581
Db 551 PIQFTSTSTRYVR-----VRYASVTSIELNVNLGNSIFTNLPATAASLDNLQS 601
QY 582 NGARFLDIN-----MGNVVA-----SDNTNVPLD-----INVTFNSGTQFEL-----MNI 621
Db 602 GDFGYVEINNAFTSATGNIVGARNFSANAIEVIDRFEFIPVTATFEAEYDLERAQKAVNA 661
QY 622 MFVPTN 627
Db 662 LFTSTN 667

RESULT 7
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE CryIIa.
GN CRYIIA.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RT "A novel CryIIa endotoxin."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 9.9%; Score 327.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 1.1e-13;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;
QY 21 HDPFSEFEHK-----SLDTIRKEW-NEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDSKISTDSLKNETDIELQINHNHEDCLKMSEYENVEFPVSASTIQTGIGIAG 68
QY 53 -IVGTVSSFLKKVGSLLIGKRISELWGLIFPSGSTNLMDILRETEQFLNQLNTDTLA 111

Db 69 KILGTLGVPPAGQVASLY-SFILGELW----PKGK-NQWEIFMEHVEEIIQKISTYARN 122

Qy 112 RVNAELEGQANIREFNQVDNFLNPTQNPVLSIT-SSVNTMQQLFLNRLPQFRVQGYQ 170

Db 123 KALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSCEE 182

Qy 171 LLLLPLFAQAAMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTYEYSNYCINTYQTA 230

Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTG 242

Qy 231 FRGL-NTRLHML---EFRTYMFNLVFEYVSIWSLKYQSLVSSGANL----YASGSGP 282

Db 243 LNNLRGTNAESWVRYNQFRRDMLMVLQVLPVPSYDTQMPYPIKTTAQLTREYVYDAIGT 302

Qy 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313

Db 303 VHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNWGG 362

Qy 314 ARLTQTFPNIGGLPGTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLLTPEV 373

Db 363 HKL--EFRTIGGTNLNIST-----QGSTNTSINPVTLPFT 394

Qy 374 RSWLDSGSDRGGVNTVT-----NWQ--TESFESTLGLRCGAGTARGNSNYFPD 419

Db 395 SRDVYRTESLAGNLFLTHPVGVPVRVDFHWKFVTHPIAS-----DNFYYPG 441

Qy 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIIYA-VHE 478

Db 442 Y-----AGIGTQLQDSENELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494

Qy 479 NGTMIHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NQGDSLRFEQSNTTA 531

Db 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNTGT 543

Qy 532 RYTLRGNG-----SYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARF 586

Db 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMR-----GED 596

Qy 587 LDINMGVNVASDNTNVPLDINVT-----FNSGTQFELMNMIFVPTNL 628

Db 597 LDYKTRFTVGTFTPFSLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVVPVEV 645

RESULT 8

O85796 PRELIMINARY; PRT; 719 AA.

AC O85796;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Insecticidal protein.

GN CRYV101.

OS Bacillus thuringiensis (subsp. kurstaki).

OG Plasmid large plasmid.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=29339;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S101;

RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF076953; AAC26910.1; --

DR HSP; P02965; 1CIY.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF00555; endotoxin; 1.

DR Pfam; PF03944; endotoxin_C; 1.

DR Pfam; PF03945; endotoxin_N; 1.

KW Plasmid.

SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 9.8%; Score 325.5; DB 2; Length 719;

Best Local Similarity 22.7%; Pred. No. 1.6e-13;

Matches 161; Conservative 103; Mismatches 272; Indels 173; Gaps 32;

Qy 21 HDPFSEHK-----SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52

Db 9 HQSPSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPFSASTIQTGIGIAG 68

Qy 53 -IVGTVSSFLKKVGLIGKRIILSELWGLIFPSGSTNLMODILRETEQFLNQLRLNTDTLA 111

Db 69 KILGTLGVPPAGQVASLY-SFILGELW---PKGK-NQWEIFMEHVEEIIQKISTYARN 122

Qy 112 RVNAELEGQANIREFNQVDNFLNPTQNPVLSIT-SSVNTMQQLFLNRLPQFRVQGYQ 170

Db 123 KALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSCEE 182

Qy 171 LLLLPLFAQAAMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTYEYSNYCINTYQTA 230

Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTG 242

Qy 231 FRGL-NTRLHML---EFRTYMFNLVFEYVSIWSLKYQSLVSSGANL----YASGSGP 282

Db 243 LNNLRGTNAESWVRYNQFRRDMLMVLQVLPVPSYDTQMPYPIKTTAQLTREYVYDAIGT 302

Qy 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313

Db 303 VHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNWGG 362

Qy 314 ARLTQTFPNIGGLPGTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLLTPEV 373

Db 363 HKL--EFRTIGGTNLNIST-----QGSTNTSINPVTLPFT 394

Qy 374 RSWLDSGSDRGGVNTVT-----NWQ--TESFESTLGLRCGAGTARGNSNYFPD 419

Db 395 SRDVYRTESLAGNLFLTHPVGVPVRVDFHWKFVTHPIAS-----DNFYYPG 441

Qy 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIIYA-VHE 478

Db 442 Y-----AGIGTQLQDSENELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494

Qy 479 NGTMIHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NQGDSLRFEQSNTTA 531

Db 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNTGT 543

Qy 532 RYTLRGNG-----GNSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARF 586

Db 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMR-----GED 596

Qy 587 LDINMGVNVASDNTNVPLDINVT-----FNSGTQFELMNMIFVPTNL 628

Db 597 LDYKTRFTVGTFTPFSLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVVPVEV 645

RESULT 9

O8KY61

ID O8KY61 PRELIMINARY; PRT; 719 AA.

AC O8KY61;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Cry.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RA Porcar M., Martinez C., Caballero P.;

RT "Identification and characterization of a novel cry gene from Bacillus thuringiensis.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF278797; AAM73516.1; --

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 9.8%; Score 323.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 2.1e-13;
Matches 160; Conservative 111; Mismatches 269; Indels 165; Gaps 34;

QY 21 HDPFSFEHK-----SLDTIRKEW-MEWKRTD-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDSKSLNETDIQLQINHEDECKISEYENVEPFVSASTIQTGISIAG 68

QY 53 -IVGTVSSFLKKVGLIGKRIKILSELWGLIFPSGSTNLMDILRETEQFLNQLNLTDLA 111
Db 69 KILGTGVFPAGQVASY-SFILGELW----PKGK-NQWEIFMEHVEEINQKISTYARN 122

QY 112 RVNAELEGLOANIREFNQOVNDFLNPTONPVLPSIT-SSVNTMQQLFLNRLPQFRVQGYQ 170
Db 123 KALTDLKGGLDALAVYHESLESWVGNRKNTARSVVKSQYIALELMFVQKLPFAVSGEE 182

QY 171 LLLLPLFAQAANMHLSEFIRDVVLNADWEGISAATLRTYQNYLKNYTYEYSNYCINTYQTA 230
Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKWYSTG 242

QY 231 FRGL-NTRLHMDL---EFRTYMFLNVFVSWLSFKYQSL--VSSGANL---YASGS 280
Db 243 LNNLRGTNAESWVRYNQFRKDMTLMVLDLVALFP--SYDTLVYPIKTSQLTREYVTD 300

QY 281 GP-QQTQSFTSQDW-----PFL-----YSLFQVNSN-YVLNGF 311
Db 301 GTVHPNASFASTWYNNNAPSSTIESAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMW 360

QY 312 SGARLTQTFPNIIGLPGTTTHALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLTLP 371
Db 361 GGHRL--EFRTIGGMLNTST-----QGSTNTSINPVTLP 392

QY 372 FVRSWLDGSDRGVNTVT-----NWQ--TESFESTLGLRCGAFARGNSNYF 417
Db 393 FTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIAS-----DNFY 439

QY 418 PDYFIRNIGSVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNKIYA-V 476
Db 440 PGY-----AGIGTQDSENELPPETTPQPNYESYSHRLSHIG--LISASHVKALVYSWT 492

QY 477 HENGTMHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NQGDLSRFEQSNT 529
Db 493 HRSA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNT 541

QY 530 TARYTLRGNGN-----SYNLYLRVSSLGNSTIRVTINGRVYTASVNTTNNNDGVNDNGA 584
Db 542 GTFGDIRVNINPPFAQRYVRIRYASTTDIQFHTSINGKAINQGNFSATMNR-GEDLDYK 600

QY 585 RFLDINMGVNVASDNTNVPLDINV-TFNSGTQFELMNIMFVPTNL 628
Db 601 TERTVGFTTPFSDVQSTFTIGAWNFSGNEVYIDRIEFVPEV 645

RESULT 10

Q9F0P8
ID Q9F0P8 PRELIMINARY; PRT; 719 AA.
AC Q9F0P8;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE CrvII.
GN CrvII.
OS Bacillus thuringiensis.
OG Plasmid pBTC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BTC007;
RA Song F., Zhang J., Huang D., Li G.;
RT "The cloning of a novel cryII gene from Bacillus thuringiensis strain."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; ICIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81025 MW; 7E17481922C435E6 CRC64;

Query Match 9.6%; Score 317.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 5.4e-13;
Matches 154; Conservative 113; Mismatches 273; Indels 139; Gaps 32;

QY 19 VAHDPF--SFEHKSLDTIRKEWMEWKRTHSLYVA-PIVGTVSSFLKKVGLIGKRILS 75
Db 37 INHEDFLRMSEHSID---PFSASTIQTGIGIAGKILGTGVFPFAGQIASLY-SFILG 91

QY 76 ELWGLIFPSGSTNLMDILRETEQFLNQLNLTDLARVNAELEGLOANIREFNQOVNDFL 135
Db 92 ELW----PKGKSO-WEIFMEHVEEELIDQKISTYARNIALADLKGGLDALAVYHESLE 146

QY 136 NPTQNPVPLSIT-SSVNTMQQLFLNRLPQFRVQYQLLLPLFAQAANMHLSEFIRDVVLN 194
Db 147 KNRNARATSVVKSQYIALELLEFVQKLPFAVSGEEVPLLPPIYAQAANLHLLLRDAS 206

QY 195 ADEWGISAATLRTYQNYLKNYTYEYSNYCINTYQTAFRGL-NTRLHMDL---EFRTYMFL 250
Db 207 GKEWGLSNSQISTFYNRQVERSDYSDHCVKWYSTGLNLRGTNAESWVRYNQFRKDMT 266

QY 251 NVFEYVSIWSLFKYQSL--VSSGANL---YASGSGP-QQTQSFTSQDW----- 293
Db 267 MVLDLIALFP--SYDTLVYPIKTSQLTREYVTDAGTVHPNASFASTWYNNNAPSFS 324

QY 294 -----PFL-----YSLFQVNSN-YVLNGFSGARLTQTFPNIIGLPGTTTHAL 335
Db 325 IESAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHRL--EFRTIGVLTNTST--- 378

QY 336 LAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLTFFVRSWLDGSDRGVNTVT----- 390
Db 379 -----QGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN 416

QY 391 -----NWQTESFESTLGLRCGAFARGNSNYFPDYFIRNIGSVPLVVRNEDLRRPLHY 443
Db 417 GVPVRDFHWKF---ATLPIASDNF-----YVLGY-----AGVGTQDSENELPPET 460

QY 444 NEIRNIESPSGTPGGLRAYMVSVHNRKNKIYA-VHENGTMHLAPEDYTGFTISPIHATQ 502
Db 461 TGQPNYESYSHRLSHIG--LISASHVKALVYSWTHRSA-----DRTN-TIEPNSITQ 509

QY 503 V-----NNQTRTFISEKFG-NQGDLSRFEQSNTTARYTLRGNGN-----SYNLYLRVSS 550
Db 510 IPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNTGTGFDIRVNINPPFAQRYVRIRYAS 567

QY 551 LGNSTIRVTINGRVYTASVNTTNNNDGVNDNGARFLDINMGVNVASDNTNVPLDINV-T 609
Db 568 TTDLQFHTSINGKAINQGNFSATMNR-GEDLDYKTRFTVGTTPFSDVQSTFTIGAWN 626

QY 610 FNSGTQFELMNIMFVPTNL 628
Db 627 FSSGNEVYIDRIEFVPEV 645

RESULT 11

Q9S5V8
ID Q9S5V8 PRELIMINARY; PRT; 1180 AA.
AC Q9S5V8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE BtT84A1 crystal protein (Crystal protein CryIA).
GN BtT84A1.
OS Bacillus thuringiensis, and
OS Bacillus thuringiensis (subsp. sotto).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428, 29340;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=T84A1;
RA Nagamatsu Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=T84A1;
RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of Bacillus
RT thuringiensis subsp. dendrolimus T84A1.";
RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=T84A1;
RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
RT "A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
RT thuringiensis.";
RL Agric. Biol. Chem. 48:611-619(1984).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis (subsp. sotto);
RA Zhong W.F., Cai P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
RT "A cryIA gene cloned from Bacillus thuringiensis serovar sotto.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026261; BAA77213.1; -
DR EMBL; AF510713; AAM44305.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DCE62D CRC64;

Query Match 8.5%; Score 280.5; DB 2; Length 1180;
Best Local Similarity 21.7%; Pred. No. 3.4e-10;
Matches 152; Conservative 104; Mismatches 272; Indels 173; Gaps 29;

QY 6 NGRTTICDAYNVVAHDPPSFEHKS LDTIRKEWMEWKRT--DHSLYVAPIVGTVSSFLLK 63
Db 3 NNPINICIPYNCLSD-----NPEVEVLGGERIETGYTPIDISL-----SLTQFLLS 48

QY 64 K-----VGS LIGKRI LSELWGLIFPSPGSTNLMDILRETEQFLNQLRNTDTLARVNAELEG 119
Db 49 EFVPGAGFVLG--LVDIIWGIFGPS---QWDAFLVQIEQLINQRIEFPARNQAISRLG 102

QY 120 LQ-----ANIREFNQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLL 172
Db 103 LSNLYQIYAESFREWE-----ADPTNPALREEMRIQFNDMNSALTTAIFLFAVQNYQVP 156

QY 173 LLPLFAQAANHL SFIRDVVLNADEWGISAA LRTYQNYLKNYTTESYNCINTYQTAFR 232
Db 157 LLSVYVQAANHL SVLRDVSFGQRWGFDATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216

QY 233 ---GLNTRLHML---EFRTYMFNLNVEYVSIWGLFKYQSLLVSSGANLYASGSGPQQTQ 286
Db 217 RVWGPDSR--DWVRNQFRRELTLTVLDIVALEFS-----NYDSRRYPIRTV 260

QY 287 SFTSQDWPFYLSLFQVNSNYVLNGFSGA-----RLTQTF--PNIGGLPGTTTHALLAA 338
Db 261 SOLTR-----BIYTNPVLENFDGSRFGMAQRIEQNIQRPHLMDILNIRITYTDVHR 311

QY 339 RVNYSGG--VSSGDIGAVFNQNFSCSTF-----LPPLLTP----- 371
Db 312 GFNYWSGHQITASPVG-----FSGPEFAFLFGNAGNAAPPVLVSLTGLGIFRTLSSPL 365
QY 372 FVRSWLDSDGSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDYFIRNISGVPLV 431
Db 366 YRRILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQGT-----VDSL DVI PPQ 417
QY 432 VRNEDLRRPLHY--NEIRNIESPSGTPGGLRAYVMVSHNRK---NNIYAVHE----- 478
Db 418 DNSVPPRAGFSHRLSHVTMLSOAAGAVYTLRAPTFSWQHRSAEFNNIIPSSQITQIPLTK 477
QY 479 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTTARY 533
Db 478 STNLGSGTSVWVKG P-----GFT-----GGDILR--RTSPGQIS 508
QY 534 TLRGN-----GNSYNLYLRVSSILGNSTIRVTINGRVYTASNVTNTNNDGVNDNGARFLD 588
Db 509 TLRVNTAPLSQRYRVIRYASTTNLQFHTSIDGRPINQGNFSATMSS-GSNLQSGSFRT 567
QY 589 INMGVVASDNTNVPLDINV-TFNSGTQFELNMIMFVPTNL 628
Db 568 VGFTTFFNFSNGSSVFTLSAHVNSGNEVYIDRIEFVPAEV 608

RESULT 12
Q9S603
ID Q9S603 PRELIMINARY; PRT; 645 AA.
AC Q9S603;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Delta-endotoxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serovar japonensis type;
RX MEDLINE=99025985; PubMed=9806979;
RA Wasano N., Ohba M.;
RT "Assignment of delta-endotoxin genes of the four lepidoptera-specific
RT Bacillus thuringiensis strains that produce spherical parasporal
RT inclusions.";
RL Curr. Microbiol. 37:408-411(1998).
DR EMBL; AF042733; AAB97923.1; -
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
FT NON_TER 1 1
FT NON_TER 645 645
SQ SEQUENCE 645 AA; 72967 MW; 143E51312B890CE3 CRC64;

Query Match 8.4%; Score 279.5; DB 2; Length 645;
Best Local Similarity 22.1%; Pred. No. 1.7e-10;
Matches 149; Conservative 94; Mismatches 276; Indels 155; Gaps 28;

QY 13 CDAYNVVAHDPPSFEHKS LDTIRKEWMEWKRTDHSLYVAPIVG---TVSSFLKKVGS LI 69
Db 4 CPADDVVKYPLTDDPNAGLQNM--NYKEYLQTYGGDYTDPLINPLNSVSGKDVIQVGINI 61

QY 70 GKRI LS-----ELWGLIFPSPGSTNLMDILRETEQFLNQLRNTDTLARVN 114
Db 62 VGRLLSFFGFPFSSQWTVVTVYLLNSLWPDDENSVWDAFMRVEBELIDQKISEAVKGRAL 121

QY 115 AELEGLOANIREFNQOVNDNFNPTQNPVPLSITSSVNTMQQLFLNRLPQF---RVQGYQ 170
Db 122 DDLTGLQYNLYVEALDEWLNRPNGARASLVSQRFNILDLSLFTQFMPSFGSGPGSQNYA 181

QY 171 LLLPLFAQAAMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTTTEYSNYCINTYOTA 230
Db 182 TILLPVYAQAANLHLLKADIIYGARWGLNQIDQFHSRQOSLTQTYNHCVTAYNDG 241
QY 231 FRGL-NTRLHDMLEFRTY--MFLNVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQ 286
Db 242 LAELRGTTAESWPKYQYRREMTLTAMDV--ALFPYNYL-----RQYDGTNPQLTR 292
QY 287 SF-----TSQ---DW-----PFLY---SLFQVNSN 305
Db 293 EYVTDPIAFDPLEQFTQLCRSWYINPAFRNHLNFSVLENSLIRPPHFLERLSNLQILVN 352
QY 306 YVLNG--FSGARLTQTFNPNGIGLPGTTTTTHALLAARVNYSGVSSGDIAGVFNQNFSCST 363
Db 353 YQTNGSAWRGSRVRYHYLHSSII--QEKSYGLLSDPVGANINVQNNDIYQIISQ---VSN 407
QY 364 FLPLLLTPF---VRSWLDSDSGDRG-----GVNTVTNWQTESFESTLGLRCGAFTARG 412
Db 408 FASPVGSSYSVWDTNPFYLSGQVSGISGYTOQGIPAVCLQQRNSTDELPSLNPEGDIIRN 467
QY 413 NS---NYFPDY-FIRNISGVPLV-----RNEDLRRPLHYNEIRNI-----ES 451
Db 468 YSHRLSHITQYRFOATQSGSPSTVSANLPTCVWTHRDVDLNTITANOITQLPLVKAYEL 527
QY 452 PSG-----TPGGLRAYMVSVHNRKNYIAVHENGTMHILAPEDYTG 493
Db 528 SSGATVVKGPFTGVDVIRRTNTGGFAGAIRVSVTGPLTQRYRIR----FRYASTIDFDF 583
QY 494 TISPIHATQVNN--QTRTFISEKFGNQDSLRFEQSNTTARYTLRGNGSNLYLVRVSSL 551
Db 584 VTR--GGTTINNFRFRTM-----NRQESRYE-SYRTVEFTTPPNFTQSQDIIRTSIQ 634
QY 552 GNSTIRVTINGRVY 565
Db 635 GLSG-----NGEVY 643

RESULT 13
Q93NM5 PRELIMINARY; PRT; 1228 AA.
ID Q93NM5
AC Q93NM5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CrylBa.
GN CRY1BA.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RF SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; --
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139666 MW; E86D9842341FB439 CRC64;

Query Match 8.4%; Score 278.5; DB 2; Length 1228;
Best Local Similarity 22.1%; Pred. No. 4.8e-10;
Matches 152; Conservative 100; Mismatches 228; Indels 209; Gaps 33;
QY 52 PIVGTVSSFLKKVSLIGKRLSELWGLIFPFGSGSTNMQDILRETEQFLNQRLNTDTLA 111
Db 68 PFAGQLASFYSFLVG-----ELW-----PRG-RDQWEIFLHVQLINQITENARN 113
QY 112 RVNAELEGLOANIREFNQVDFNLPNTQNPVPLSITSSVNTMQQL-FLNRLPQFRVQGYQ 170
Db 114 TALARLQGLGDSFRAYQQSLEDWLENRDDRTRSVLYTQYIALELDPLNAMPFLFAIRNQE 173

QY 171 LLLPLFAQAAMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTTTEYSNYCINTYOT- 229
Db 174 VPLLVMVYAQAANLHLLRDASLFCSEFGLTSQEIQRYVERQVTRDRYSDYCVWEYNTG 233
QY 230 --AFRGLN---TRLHDMLEFRTYMFNVFVYSIWSLFKYQSLVSSGANL-----YASG 279
Db 234 LNSLRGTNAASWVRYN--QFRDLTLGLVLDLVALFPSYDTRYPINTSAQLTREYVYTD 290
QY 280 SGPOQTQSFTSQDW-----PFL-----YSLFQVNSNYV-----LNGF 311
Db 291 IGATGV-NMASMNWYNNNAPSFAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYW 349
QY 312 SGARLTQTFNPNGIGLPGTTTTTHALLAARVN-----YSGGVSSGDIAGVF 355
Db 350 RG-RTIQSRPIGGGL--NTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLWG----- 400
QY 356 NONFSCSTFLPPLLTTPFVRSWLDSDSGDRGVNTV---TNWQTESFESTLGLRCGAFTAR 411
Db 401 -----IYLEPI-----HGVPTVRFNFTNPQN-----ISDR 425
QY 412 GNSNYFPDYPFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKN 471
Db 426 GTANYSQPY-----ESPGQLKXDSLETLPETTERPNYESYSHR---LSHIGIILQSRVN 477
QY 472 -NIYA-VHENGTMHILAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDSLRFEQSNT 529
Db 478 VPVYSWTHRSA-----DRTN-TIGPNRITQI-----PMVKASELPQGTTV----- 516
QY 530 TARYTLRGNG-NSYNLYLVRVSSLSGNSTIRVTNG-----RVYTASNVTNTTNDG 578
Db 517 -----VRGPGFTGGDILRRNTGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGG 571
QY 579 VNDNGARFL-----DINMGVV-----ASDNTNVPLD--- 605
Db 572 TTVNNFRFLRMTMSGDELKYGNFVRRAPTTPFTTQIQDIIRTSIQSLSGNGEVYIDKIE 631
QY 606 -INVTFSNGTQFEL-----NMIMFVPTN 627
Db 632 IIPVTATFEAEYDLERAQEAVALFTNTN 660

RESULT 14
Q45740 PRELIMINARY; PRT; 381 AA.
ID Q45740
AC Q45740
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Insecticidal crystal protein (CryIF) (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN=EG6346;
RX MEDLINE=91286178; PubMed=2061280;
RA Chambers J.A., Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,
RA Gawron-Burke C.;
RT "Isolation and characterization of a novel insecticidal crystal
RT protein gene from Bacillus thuringiensis subsp. aizawai.";
RL J. Bacteriol. 173:3966-3976(1991).
DR EMBL; M63897; AAA22349.1; --
DR HSSP; P07130; 1DLCL
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03945; endotoxin_N; 1.
FT NON TER 381
SQ SEQUENCE 381 AA; 42967 MW; DDAEF0D0504CE96C CRC64;
Query Match 8.4%; Score 277.5; DB 2; Length 381;
Best Local Similarity 26.3%; Pred. No. 1.1e-10;

Matches 100; Conservative 66; Mismatches 135; Indels 79; Gaps 19;

Qy 21 HDPFSFEHK---SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52

Db 9 HQSFSSNAKVDKISTDSKNETDIELQINHEDECLKISEYENVEPFVSASTIQTGISIAG 68

Qy 53 -IVGTSSFLKKVGLICKRILSELWGLIFPSSGSTNMQDILRETEQFLNQLRNTDTLA 111

Db 69 KILGTLGVPEAGQVSLY-SFILGELW-----PKGK-NQWEIFMEHVEEIIINOKISTYARN 122

Qy 112 RVNAELEGLOANIREFNQVDNFLNPTQNPVPLSIT-SSVNTMQQLFLNRLPQFRVQGYQ 170

Db 123 KALTDKGLGDALAVYHESLESWVGNRKNTRARSVVKSQYIALELMFVQKLPFAVSGEE 182

Qy 171 LLLPLFAQAANMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTYEYSNYCINTYQTA 230

Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTG 242

Qy 231 FRGL-NTRLHML---EFRTYMFLNVFEYVSIWSLFKYQSL--VSSGANL---YASGS 280

Db 243 LNNLRGTNAESWVRYNQFRKDMTLMVLDLVALFP--SYDTLVYPIKTSQLTREYTTDAI 300

Qy 281 GP-QQTQSFTSQDW-----PFL-----YSLFQVNSN-YVLNGF 311

Db 301 GTVHPNASFASWTWYNNNAPSFTIESAVVRNPHLLDFLEQVTIYSLLSRWSNTQYVMNW 360

Qy 312 SGARLTQTFNIGGLPGTTT 331

Db 361 GGHL--EFRTIGGMLNTST 378

RESULT 15

Q45720 PRELIMINARY; PRT; 620 AA.

AC Q45720;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE CryIA(a) (Fragment).

GN CryIA(A).

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NRD-12;

RX MEDLINE=95386467; PubMed=7657602;

RA Masson L., Lu Y.J., Mazza A., Brousseau R., Adang M.J.;

RT "The CryIA(c) receptor purified from Manduca sexta displays multiple specificities.";

RL J. Biol. Chem. 270:20309-20315(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NRD-12;

RX MEDLINE=95231292; PubMed=7715447;

RA Masson L., Mazza A., Gringorten L., Baines D., Aneliunas V., Brousseau R.;

RT "Specificity domain localization of Bacillus thuringiensis insecticidal toxins is highly dependent on the bioassay system.";

RL Mol. Microbiol. 14:851-860(1994).

DR EMBL; U43605; AAA86265.1; -.

DR HSSP; P02965; ICIY.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF00555; endotoxin; 1.

DR Pfam; PF03944; endotoxin_C; 1.

DR Pfam; PF03945; endotoxin_N; 1.

FT NON_TER 1

FT NON_TER 620

SQ SEQUENCE 620 AA; 69428 MW; 4571A09E56E56EDE CRC64;

Query Match

8.3%; Score 276.5; DB 2; Length 620;

Best Local Similarity 21.5%; Pred. No. 2.5e-10;

Matches 151; Conservative 105; Mismatches 272; Indels 173; Gaps 29;

Qy 6 NNGRTTICDAYNVVAHDPFSEHKSLDTIRKEWMEWKT--DHSLYVAPIVGTVSSFLK 63

Db 3 NNPINECIPYNCLS-----NPEVEVLGGERIETGYTPIDISL-----SLTQFLS 48

Qy 64 K----VGLIGKILSELWGLIFPSSGSTNMQDILRETEQFLNQLRNTDTLARVNAELEG 119

Db 49 EFVPGAGFVLG--LVDIIWGIFGPS---QWDAFLVQIEQLINQRIEEFARNQAISRLG 102

Qy 120 LQ-----ANIREFNQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLL 172

Db 103 LSNLYQIYAESFREWE-----ADPTNPALREEMRIQFNDMNSALTTAIPLLAQVNYQVP 156

Qy 173 LLLPLFAQAANMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTYEYSNYCINTYQTA 232

Db 157 LLSVYVQAANLHLSVLDRVSVFGQRWGFDAAATINSRYNDLTRIGNYTDYAVRWYNTGLE 216

Qy 233 ---GLNTRLHML---EFRTYMFLNVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQ 286

Db 217 RVWGPDSR--DWVRYNQFRRLTLVLDIVALFS-----NYDSRRYPPIRTV 260

Qy 287 SFTSQDWPFYLSLFQVNSNYVLNGFSGA-----RLTQTF--PNIGGLPGTTTHALLAA 338

Db 261 SQLTR-----EITYNPVLENFDFGSFRGMAQRIEQNRQPHLMDILNSITIYTDVHR 311

Qy 339 RVNYSGG--VSSGDIGAVENQNFSCSTF-----LPPLLT----- 371

Db 312 GFNYWSGHQITASPVG-----FSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPL 365

Qy 372 FVRSWLDSGSDRGVNTVTNMQTESFESTLGLRCGAFARGNSNYFPDYFIRNISGVPLV 431

Db 366 YRRILGSGPNQELFVLDGTGFESFASLTNLPSTIYRQGT-----VDSLDPVIPPQ 417

Qy 432 VRNEDLRRPLHY--NEIRNIESPSGTPGGLRAYMVSVNRK---NNIYAVHE----- 478

Db 418 DNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAPTFSWQHRSAEFNIIIPSSQITQIPLTK 477

Qy 479 ----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRFESQNTTARY 533

Db 478 STNLGSGTSVVKGP---GFT-----GGDILR--RTSPGQIS 508

Qy 534 TLRGN-----GNSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTNNDGVNDNGARFLD 588

Db 509 TLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFBSATMSS--GSNLQSGSFT 567

Qy 589 INMGNVVASDNTNVPLDINV-TFNSGTQFELMNMIFVPTNL 628

Db 568 VGFTTFEFSNGSSVFTLSAHVFNSEVYIDRIEFVPAEV 608

Search completed: December 12, 2003, 16:17:37

Job time : 42 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 12, 2003, 16:10:35 ; Search time 17 Seconds
(without alignments)
1748.287 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
Sequence: 1 MNNVLNNGRTTICDAYNVVA.....GTQFELMNMIFVPTNLPPIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3048.5	92.0	633	1 C2AA_BACTK	P21253 bacillus th
2	3010.5	90.8	633	1 C2AB_BACTK	P21254 bacillus th
3	2916.5	88.0	633	1 C2AD_BACTU	Q9rmg3 bacillus th
4	2545	76.8	622	1 C2AC_BACTU	Q45743 bacillus th
5	1087	32.8	675	1 C1BA_PAEPP	P57091 paenibacill
6	1080	32.6	706	1 C1AA_PAEPP	Q45358 paenibacill
7	1073.5	32.4	695	1 C1CA_PAEPP	P57092 paenibacill
8	336.5	10.2	643	1 CBA_A_BACTI	P21256 bacillus th
9	327.5	9.9	719	1 C1IA_BACTK	Q45752 bacillus th
10	327.5	9.9	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
11	325	9.8	719	1 C1ID_BACTU	Q9xd11 bacillus th
12	310.5	9.4	719	1 C1IB_BACTE	Q45709 bacillus th
13	307	9.3	1157	1 C9CA_BACTO	Q45733 bacillus th
14	306	9.2	1138	1 C7AB_BACUA	Q45707 bacillus th
15	305.5	9.2	1227	1 C1BE_BACTU	O85805 bacillus th
16	304.5	9.2	750	1 CBBB_BACTV	Q9zius5 bacillus th
17	300.5	9.1	682	1 C1BA_BACUH	O86170 bacillus th
18	294.5	8.9	1176	1 C1CB_BACTG	P56953 bacillus th
19	293.5	8.9	1229	1 C1BB_BACTU	Q45739 bacillus th
20	293.5	8.9	1233	1 C1BC_BACTM	Q45774 bacillus th
21	291.5	8.8	1179	1 C1AD_BACTA	Q03744 bacillus th
22	288.5	8.7	1138	1 C7AB_BACUK	Q45708 bacillus th
23	287	8.7	724	1 CBBB_BACTJ	Q45730 bacillus th
24	282.5	8.5	1169	1 C8BA_BACUK	Q45705 bacillus th
25	280	8.4	1169	1 C9DA_BACTP	O06014 bacillus th
26	277	8.4	1181	1 C1AE_BACTL	Q03748 bacillus th
27	275.5	8.3	1170	1 C1JB_BACTU	Q45716 bacillus th
28	275.5	8.3	1228	1 C1BA_BACTK	P05517 bacillus th
29	273	8.2	1215	1 C1KA_BACTM	Q45715 bacillus th
30	272.5	8.2	826	1 CRAA_BACUH	Q9s597 bacillus th
31	271.5	8.2	1176	1 C1AA_BACTK	P02965 bacillus th
32	270.5	8.2	1174	1 C1EB_BACTA	Q03745 bacillus th
33	268	8.1	1155	1 C1AB_BACTK	P06578 bacillus th

RESULT 1
C2AA_BACTK
ID C2AA_BACTK STANDARD; PRT; 633 AA.
AC P21253; O52764;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2Aa (Insecticidal delta-endotoxin)
DE CryIIA(a)) (Crystalline entomocidal protoxin) (71 kDa crystal protein)
DE (P2 crystal protein) (Mosquito factor).
GN CRY2AA OR CRYIIA(A) OR CRYB1 OR CRYII.
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. kurstaki), and
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 33930;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=89123178; PubMed=2914879;
RA Widner W.R., Whiteley H.R.;
RT "Two highly related insecticidal crystal proteins of Bacillus
RT thuringiensis subsp. kurstaki possess different host range
RT specificities".
RL J. Bacteriol. 171:965-974 (1989).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RC SPECIES=B.t.kurstaki; STRAIN=HD-263, and HD-1;
RX MEDLINE=88087146; PubMed=3121615;
RA Donovan W.P., Dankocsik C.C., Gilbert M.P., Gawron-Burke M.C.,
RA Groat R.G., Carlton B.C.;
RT "Amino acid sequence and entomocidal activity of the P2 crystal
RT protein. An insect toxin from Bacillus thuringiensis var. kurstaki.";
RL J. Biol. Chem. 263:561-567 (1988).
RN [3]
RP REVISIONS.
RA Donovan W.P., Dankocsik C.C., Gilbert M.P., Gawron-Burke M.C.,
RA Groat R.G., Carlton B.C.;
RL J. Biol. Chem. 264:4740-4740 (1989).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kenya; STRAIN=4A4C / HD-549;
RA Miera H.S., Khairnar N.P., Mathur M., Donnelly R.J., Mahajan S.K.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF BOTH DIPTERAN (AEDES AEGYPTI) AND LEPIDOPTERAN
CC (MANDUCA SEXTA) LARVAE.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M23723; AAA83516.1; -
DR EMBL; M31738; AAA22335.1; -
DR EMBL; AF047038; AAC04867.1; -
DR PIR; C32053; C32053.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
FT VARIANT 1 1 MISSING (IN 50% OF THE MOLECULES).
FT VARIANT 3 3 N -> S (IN STRAIN 4A4C / HD-549).
FT VARIANT 409 409 F -> S (IN STRAIN 4A4C / HD-549).
FT VARIANT 541 541 N -> S (IN STRAIN 4A4C / HD-549).
FT VARIANT 588 588 S -> P (IN STRAIN 4A4C / HD-549).
SQ SEQUENCE 633 AA; 70852 MW; 15182F4C778E58A4 CRC64;

Query Match 92.0%; Score 3048.5; DB 1; Length 633;
Best Local Similarity 90.7%; Pred. No. 3.2e-198;
Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTRKEWMWKRTDHSLYVAPVGVTSVF 60
DB 1 MNNVLSGRITTCIDAYNVVAHDPFSEHKSLDTRKEWMWKRTDHSLYVAPVGVTSVF 60
QY 61 LLKKVGLIGKRIKILSELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDHLARVNAELEG 120
DB 61 LLKKVGLIGKRIKILSELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDHLARVNAELEG 120
QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQVQLLLPLFAQA 180
DB 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQVQLLLPLFAQA 180
QY 181 ANMHLSFIRDVILNADWEGISAATLRTYQNYLKNYTTYSNYCINTYQTAFLRGLNRLHD 240
DB 181 ANMHLSFIRDVILNADWEGISAATLRTYQNYLKNYTTYSNYCINTYQTAFLRGLNRLHD 240
QY 241 MLEFRTYMFNVFYSIWSLFKYQSLVSSGANLYASGGPQQTQSFTSDWPFLYSLF 300
DB 241 MLEFRTYMFNVFYSIWSLFKYQSLVSSGANLYASGGPQQTQSFTSDWPFLYSLF 300
QY 301 QVNSNYLVNGFSGARLTQTFEPNIGLPGTTTHALLAARVNSGGVSSGDIGAV-FNQNF 359
DB 301 QVNSNYLVNGFSGARLTQTFEPNIGLPGTTTHALLAARVNSGGVSSGDIGAV-FNQNF 359
QY 360 SCSTFLPPLLTTPFVRSWLDGSDRGVNTVNTWQTESPESTLGLRCGAFARGNSNYFPD 419
DB 361 NCSTVLPLPLSTPFVRSWLDGSDRGVNTVNTWQTESPESTLGLRCGAFARGNSNYFPD 420
QY 420 YFIRNIGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNKIYAVHEN 479
DB 421 YFIRNIGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNKIYAVHEN 480
QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNRTARYTLRNG 539
DB 481 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNRTARYTLRNG 540
QY 540 NSYNLYLRVSSLGNTSTIRVTINGRVYTASVNTTNNNDGVNDNGARFLDINMGNVASDN 599
DB 541 NSYNLYLRVSSLGNTSTIRVTINGRVYTASVNTTNNNDGVNDNGARFLDINMGNVASDN 600
QY 600 TNVPLDINVTNSGTFQFELNMIMFVPTNLPPIY 632
DB 601 TNVPLDINVTNSGTFQFELNMIMFVPTNLPPIY 633

RESULT 2
C2AB_BACTK STANDARD; PRT; 633 AA.
ID_C2AB_BACTK

AC P21254;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2Ab (Insecticidal delta-endotoxin
DE CryIIA(b)) (Crystalline entomocidal protoxin) (71 kDa crystal protein).
GN CRY2AB OR CRYIIA(B) OR CRYB2.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1;
RX MEDLINE=89123178; PubMed=2914879;
RA Widner W.R., Whiteley H.R.;
RT "Two highly related insecticidal crystal proteins of Bacillus
RT thuringiensis subsp. kurstaki possess different host range
RT specificities.";
RL J. Bacteriol. 171:965-974 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91211618; PubMed=2089222;
RA Dankocsik C.C., Donovan W.P., Jany C.S.;
RT "Activation of a cryptic crystal protein gene of Bacillus
RT thuringiensis subsp. kurstaki by gene fusion and determination of
RT the crystal protein insecticidal specificity.";
RL Mol. Microbiol. 4:2087-2094 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC002;
RA Chen Z.Y., Zhang J., Huang D.F.;
RT "Bacillus thuringiensis Btc002 cry2Ab gene.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERAN (MANDUCA SEXTA) LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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DR EMBL; M23724; AAA22342.1; -
DR EMBL; X55416; CAA39075.1; -
DR EMBL; AF164666; AAG36762.1; -
DR PIR; D32053; D32053.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 633 AA; 70741 MW; 424B937DFDDF3D61 CRC64;

Query Match 90.8%; Score 3010.5; DB 1; Length 633;
Best Local Similarity 89.7%; Pred. No. 1.2e-195;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTRKEWMWKRTDHSLYVAPVGVTSVF 60
DB 1 MNNVLSGRITTCIDAYNVVAHDPFSEHKSLDTRKEWMWKRTDHSLYVAPVGVTSVF 60
QY 61 LLKKVGLIGKRIKILSELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDHLARVNAELEG 120
DB 61 LLKKVGLIGKRIKILSELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDHLARVNAELEG 120

RC STRAIN=Shanghai 1 / S-1;
RX MEDLINE=91340086; PubMed=1651878;
RA Wu D., Cao X.L., Bai Y.Y., Aronson A.I.;
RT "Sequence of an operon containing a novel delta-endotoxin gene from
RT Bacillus thuringiensis";
RL FEMS Microbiol. Lett. 65:31-36(1991).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. HAS LOW ACTIVITY ON
CC DIPTERAN LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC -----
DR EMBL; X57252; CAA40536.1; -.
DR PIR; S17402; S17402.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation; Plasmid.
SQ SEQUENCE 622 AA; 69729 MW; E0BE5FAD37BF8299 CRC64;

Query Match 76.8%; Score 2545; DB 1; Length 622;
Best Local Similarity 78.9%; Pred. No. 2.9e-164;
Matches 501; Conservative 45; Mismatches 73; Indels 16; Gaps 8;

QY 1 MNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTSSVF 60
Db 1 MNTVLNNGRNTTCHAHNVVAHDPPSFSEHKSLNTEKEWKRTDHSLYVAPIVGTGSPF 60

QY 61 LLKKVGSGLIGKRILSELWGLIFPSSGNTLMQDILRETEQFLNQLNTDTLARVNAELEG 120
Db 61 LLKKVGSGLVGRILSELQNLIFPSSGIDLMQEIILRATEQFINQLNADTLGRVNAELAG 120

QY 121 QANIREFNQVQVDNFTNPTQNPVPLSITSSVNTTMOQLFLNLPQFRVQGYQLLLPLFAQ 180
Db 121 QANVAEFNRQVDNFTNPNQNPVPLAIDSNTLQQLFLSRLPQFQIQGYQLLLPLFAQ 180

QY 181 ANMHLSFIRDVVLNADWGISAAATLRTYQNYLKNYTYEYSNYCINTYQTAFRGLNRLHD 240
Db 181 ANFNLSFIRGVILNADWGISAAATVTRYDRHLRKFHRDYSNYCINPYQTAFRGLNRLPD 240

QY 241 MLEFRTYMFNLNVEFVSIWSLKFYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
Db 241 MLEFRTYMFNLNVEFVSIWSLKFYQSLVSSGANLYASGSGP--TQSFTAQNPFLYSLF 298

QY 301 QVNSNYVLNFGFSGARLTQTFPNIIGLP--GTTTHALLAARVNSYGGVSSGDIG-AVFNQ 357
Db 299 QVNSNYVLNGLSGARTTITFPNIGGLPVYHNSTLH--FARINRYGGVSSSRIGQANLNQ 355

QY 358 NFSCSTFLPPLTTPFVRSWLDGSDRGVNTVTNQWTFESFESTLGRCCGAPTARGNSNYF 417
Db 356 NFNISTLFNPLQTPFIRSWLDGSDTREGVATSNWQSGAFETTL-LRFSTFSARGNSNF 414

QY 418 PDYFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYIAVH 477
Db 415 PDYFIRNISGVVGTISNADLARPLHFEIRDI----GTTA--VASLVTVHNRKNYIDTH 468

QY 478 ENGTMHILAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFESQNTTARYTLRG 537
Db 469 ENGTMHILAPNDYTGFTVSPHATQVNNQIRTFISEKYGNGQDSLRFELSNPTARYTLRG 528

QY 538 NGNSYNLYLRVSSLSGNSTIRVTINGRVVYTAASNVTNTTNDGVNDNGARFLDNMGNVVAS 597
Db 529 NGNSYNLYLRVSSLSGSSSTIRVTINGRVVYTA-NVNTTNDGVLDNGARFSDINIGNVAS 587

QY 598 DNTNVPLDINVTFTSGTQFELMNMIFVPTNLPPIY 632
Db 588 ANTNPVLDIQVTFNGNPOFELMNMIFVPTNLPPLY 622

RESULT 5
CIBA_PAEPP STANDARD; PRT; 675 AA.
ID CIBA_PAEPP AC PS7091;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cry18Ba (Parasporal delta-endotoxin
DE CryXVIII(a)) (Crystalline parasporal protoxin) (76 kDa crystal
DE protein).
GN CRY18BA OR CRYXVIII(A).
OS Paenibacillus popilliae (Bacillus popilliae).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=78057;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP3;
RA Patel R., Yousten A.A., Rippere K.;
RT "Detection of two new cry genes in Paenibacillus popilliae.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P.POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF169250; AAF89667.1; -.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
FT DOMAIN 101 104 POLY-LEU.
FT DOMAIN 199 204 POLY-LEU.
SQ SEQUENCE 675 AA; 75848 MW; 823B588B4AE81DF5 CRC64;

Query Match 32.8%; Score 1087; DB 1; Length 675;
Best Local Similarity 38.9%; Pred. No. 7.3e-66;
Matches 259; Conservative 104; Mismatches 244; Indels 58; Gaps 19;

QY 2 NNVL-NNGRTTICDAYNVVAHDPPSFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTSSVF 60
Db 35 NNIICSGFMPI---NVTRKNP--FRKRTTQEFIRETWEKENSPLFTAPIVGVVTS 88

QY 61 LLKKVGSGLIGKRILSELWGLIFPSSGNTLMQDILRETEQFLNQLNTDTLARVNAELEG 120
Db 89 LLEALKKQVQSRLLLMTNLLFPNNSTSTMEILRATEQYVQGLDVTWNRVSOELEG 148

QY 121 QANIREFNQVQVDNFTNPTQNPVPLSITS---SVNTMQQLFLNLPQFRVQGYQLLLPLF 177
Db 149 KNNLRTFNDQIDDFL---QNRVEISPTAMIDSINTMQQVFNRLPQFQLSDYQLLLPLF 205

QY 178 AQANMHLSFIRDVVLNADWGISAAATLRTYQNYLKNYTYEYSNYCINTYQTAFRGL--- 234

Db 206 AQGATLHLTfirdiIINAGEwnIPEaQLNtCKrYlKQYVAQYsNYalStYEGaFRaRfYP 265
QY 235 NTRLHDMLEERTYmFLNvFeyVSIwSLfKYQSLlVSSGaNLYaSGPQQTQSFTSQDWP 294
Db 266 RATLENMLQFKTfMTlNlVlDlVSIwSLlKYmNLYlStSAnLYNlGDNKvNEGEYSISYWP 325
QY 295 FLYSLFQVNSYVLNGfSGaRLTQTfPNlGGLPGTtTHAlLaARvNSYGGVSSGDIGAV 354
Db 326 FfNSYlQTkSNYlVSGVGAIRWYlNT--FFGByIQDNLNlIIASyVGVNGPKlGVQ 383
QY 355 FNQ-----NFSCSTfLpLLTPfVRsWLDSGSDRGvNTVTNW 392
Db 384 LSTTELDKQlKQARAGMPTGLDdLSfNC-TLRNPTVPYfACNFQELTSSGTAGTGGFI 442
QY 393 QTESFESTLGLRCGaFTaRGNS-NYfPDYfIRNlSG-VPLVVRNEDLRRPLHYNlEIRNlE 450
Db 443 RSDVFRSEdNI-CGLGTGYASAwTSYpDYlITNlSAtVQVDGINIdI-TPLCFGEDRAIT 500
QY 451 SPSGTPGGLRaYmVSVHNRKNlYAVHENGtMIHLAPEDYtGFTISPIHATQVNNQTRTF 510
Db 501 STHGV----NKVlAVNRKAnlAGTNQNGtMIHQAPNDGTGTvSPHLASfTHPSEAH 555
QY 511 ISEKfGNQDslRfEQSNtTARyTLRGNGNS-YNLyLRvSS-LGNStIRVtNGRVYtAS 568
Db 556 IQENYGNsgDslRLTGFTtAITyMLSGDGRtYlKlVRVSGVITRItAKVRGNSlGY-LE 614
QY 569 NVNTTNDGVNDNGARfLDlNMGNVVASD-NTNVPLDlNVtNSGTQfELNMlMFVPTN 627
Db 615 YlNTVDNNGlTNGSKfQDFEFRPTITIdAQTPlVLEfSATS-----FDLMNlIFlPY 670
QY 628 LPPIY 632
Db 671 DTPIY 675

RESULT 6
C1AA_PAEPP STANDARD; PRT; 706 AA.
AC Q45358;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cry18Aa (Parasporal delta-endotoxin
DE CryXVIIIa(a)) (Crystalline parasporal protoxin) (79 kDa crystal
DE protein).
GN CRY18AA OR CRYXVIII(A) OR CRYBP1.
OS Paenibacillus popilliae (Bacillus popilliae).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=78057;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=H1 / subsp. melolonthae;
RX MEDLINE=97352693; PubMed=9209052;
RA Zhang J., Hodgman T.C., Krieger L., Schnetter W., Schairer H.U.;
RT "Cloning and analysis of the first cry gene from Bacillus popilliae."
RL J. Bacteriol. 179:4336-4341(1997).
CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P.POPILLIAE TO ENTER THE HEMOLYMPH. ACTIVE ON
CC M.MELOLONTHA.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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DR EMBL; X99049; CAA67506.1; --
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
FT CONFLICT 670 T -> F (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 706 AA; 79034 MW; 9172B949BE499C1D CRC64;

Query Match 32.6%; Score 1080; DB 1; Length 706;
Best Local Similarity 38.4%; Pred.No. 2.3e-65;
Matches 264; Conservative 96; Mismatches 233; Indels 94; Gaps 21;

QY 2 NNVLNN-----GRttICDA----YNVVAHDpFSEHKSLDTIRKEWMEWKRtD 45
Db 58 NNDNNDAICDELGLTPIDNNTICSTdFTPINVMRTDP--FRKkStQELtREWtEWKENS 115
QY 46 HSlyVAPIvGTvSSFLlKKVGSliGKRilSELWGLlFPpSGStNlMQDilREtEQFLNQRl 105
Db 116 PSLfTPAlVGvVtSfLLQSLKkQATsFLlKtLTdLLfPNNSSlTMEElRAtEQYVQERl 175
QY 106 NTdTLARvNAElGLQAnlREfNQVDNfLNpTQNpVPLsITSSvNTMQQLfLNRLPQFR 165
Db 176 DTDtANRVsQELVGLKNNLTtFNdQVEDfLQNRVGlSPlAlIdStNTMQQLfVNRlPQFQ 235
QY 166 VQGYQlLLlPLPaQAAmHLsFIRdVVLNAdEWGIsAATLRtYQNLKNTYtEYSNYCIN 225
Db 236 VSGYQVLLlPLPaQAATLHLtFLRDvIINAdEWNIPTAQlNTYtRYfKEyIAEYSNYALS 295
QY 226 TyQTAFRGlnTR-----LHDMLEfRTYmFLNvFeyVSIwSLfKYQSLlVSSGaNLYaSG 279
Db 296 TyDDGFR--TRfYPRNTLEdMLQFKTfMTlNALDlVSIwSLlKYVNLyVStSANLYNlG 352
QY 280 SGpQQTQSFTSQDWPfLYSLfQVNSYVLNGfSGaRLTQTfPNlG-----LPgTtTtH 333
Db 353 DNKvNEGAYPIsYGPfFNSYlQTkSNYlVSGVSGlGARfYtStVGLRYlHDDlKNIItT- 411
QY 334 ALLaARvNSYGGVSSGDIGAVN-----QNfSCSTfLP-PLlTLP 371
Db 412 -----YVGtQGPNlGVQLStELdELKkQQAtrDslVDfQfFTlNCMLPNlPITAP 463
QY 372 -FvRSWlDSG-SDRGvNTVTNMQTESfESTlGL-RCGaFTaRGNSYfPDYfIRNlSGV 428
Db 464 YfATsLYESRYSSlGGYlRKdVfKSE--DStCGLNGPGAwTS-----YpDYlITNlSAT 515
QY 429 PLVVRNEDLRRPLHYNlEIRNlESpSGTPGGLRaYmVSVHNRKNlYAVHENGtMIHLAPe 488
Db 516 VQlNGENTdTTPlyfKEnRPITSTRGV-----NKVlAVNRKAnlAGTNQNGtMIHQAPP 570
QY 489 DYtGFTISPIHATQVNNQTRTfISEKfGNQDslRfEQSNtTARyTLRGNG-NSYNLYLR 547
Db 571 DGTGTvSPLHPsA--NTITSYlKENYGNsgDslHL-KGQGYLHylMlSGNGQDRYRLVLR 627
QY 548 VSSlGNStIRVtNGRVYtASNVNTTNDGVNDNGARfLDlNMGN--VVASDNTNVPLD 605
Db 628 LSGAAN---QlKLQSPtTSIYAFDTStNNEGITDNGSKfKDFAFStPFVlPEQK-----E 679
QY 606 INVTfNSGTQfELNMlMFVPTNLPPIY 632
Db 680 lVlyfEGVGSldLMNlIFLPADDTPLY 706

RESULT 7
C1CA_PAEPP STANDARD; PRT; 695 AA.
ID C1CA_PAEPP
AC P57092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cry18Ca (Parasporal delta-endotoxin
DE CryXVIIIc(a)) (Crystalline parasporal protoxin) (78 kDa crystal

DE protein).
GN CRY18CA OR CRYXVIIIC(A).
OS Paenibacillus popilliae (Bacillus popilliae).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=78057;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14706;
RA Patel R., Yousten A.A., Rippere K.;
RT "Detection of two new cry genes in Paenibacillus popilliae.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P.POPILLIAE TO ENTER THE HEMOLYPH (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF169251; AAF89668.1; -.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 695 AA; 78259 MW; 406AC9154D75E070 CRC64;

Query Match 32.4%; Score 1073.5; DB 1; Length 695;
Best Local Similarity 37.6%; Pred. No. 6.2e-65;
Matches 256; Conservative 115; Mismatches 241; Indels 69; Gaps 18;

QY 2 NNV-----LNNGRTTICDAY-----NNVAHDPFSEHKSLDTRKEWMEWKRTDHS 47
DB 34 NNVNRGDLVTNGLTPIIDNNFISNGFIPRNVTRKDP--FRKRTTQEFIREWTEWKEKSAS 91

QY 48 LVVAPIGVTVSSFLKVKVSLGKRLSELWGLIPSPSGSTNMQDLRETEQFLNQLRINT 107
DB 92 LFTAPIGVITSTLLEALKKLVAGRVLSLTNLLFPNNSTSTMBEILRATEQYIQEQLDT 151

QY 108 DTLARVNAELEGLOANREFNQVDNLFNPTQNVPLSITSSVNTMQQLFNRLPQFRVQ 167
DB 152 VTNRVSOELEGKNDLRTFNQDIDFLQNRVGSPLAIDSINTMQQLFNRLPQFQVS 211

QY 168 GYQLLLPLFAQAANMHLSPFIRDVVLNADENWISAAATLRTYQNYLKNYTEYSNYCINTY 227
DB 212 DDQVLLPLFAQAVTLHLTFVRDIIINADENWIPEAQLNTYKRYLKQYVAQYSNYALSTY 271

QY 228 QTAFRG---LNRHDMLEFRTYMFLNVFYSIWSLKYQSLVSSGANLYASGSGPQ 283
DB 272 EEAFRARFYPRNT--VENMLEFKTFMTNLNVLDSVMSLLKYVNLVYSTANLYNIGDNKV 330

QY 284 QTSFTSQDWPFYSLFQVNSNYVLNGFSGARLTQTFPN-----IGG 325
DB 331 NEGEYSISYWPFFNTYIQTNSYVLGVSQGYAMRWSTNPFGEYIQDHLNITASYIGG 390

QY 326 LPG-----TTTTHALLAARVNSYSGVSSGDIQAVENQNFSCSTFLPPLLTFFVRSWL 377
DB 391 VNGPQIGQQLSTTELDQLVQQQ-----ARADIPVDFTQIPINCLRNPLEVPYYATRF 443

QY 378 DSGSDRGGVNTVNTWQTESPESTGLRCGAF--ARGNSNYFPDYFIRNIGS-VPLVVRNE 435
DB 444 NELTSLGTAGVGGFVRSDVFISNDSV-CGLGTYSSGQTFPDYITNISATVQVNGTNT 502

QY 436 DLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIIYAVHEN--GTMIHLAPEDYTG 493

Db 503 DI-SPLYFGENRAITSTNGV-----NKVIAIYNRKTN-YDDFTNIRGTIVHEAPTDTSTGF 555
QY 494 TISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNNTTARYTL-RGNNSYNLYLRVSSLG 552
DB 556 TISPLHLDTVNINSYLYIQENYGNNGDSLVR-INRAIIKYRLSAARSVIYRLVLRVSGTA 614
QY 553 NSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDNTNVPLDINVT-FN 611
DB 615 SSIVAIYENYPVGSANQINTGTNEGVIDNDSKFIDLIFNTPTFVSVSGTARELQOVSGAT 674
QY 612 SGTQFELMNMVPTNLPPY 632
DB 675 TSSPLDMMNIIIPINDVPLY 695

RESULT 8
CBAA_BACTI STANDARD; PRT; 643 AA.
AC P21256;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIIAa (Insecticidal delta-endotoxin
DE CryXIA(a)) (Crystalline entomocidal protoxin) (72 kDa crystal protein).
GN CRYIIAA OR CRYXIA(A) OR CRYIIVD OR CRYD.
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89008093; PubMed=2902069;
RA Donovan W.P., Dankocsik C.C., Gilbert M.P.;
RT "Molecular characterization of a gene encoding a 72-kilodalton
RT mosquito-toxic crystal protein from Bacillus thuringiensis subsp.
RT israelensis";
RL J. Bacteriol. 170:4732-4738(1988).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MOSQUITOS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31737; AAA22352.1; -.
DR PIR; A43647; A43647.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 643 AA; 72348 MW; 64CA35495409B74E CRC64;

Query Match 10.2%; Score 336.5; DB 1; Length 643;
Best Local Similarity 23.1%; Pred. No. 2.9e-15;
Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;

QY 27 EHKSLLDTRKEWMEWKRTDHSLY-----VAP---IVGVSSFLKVKVSLGKRLSE 76
DB 2 EDSSLDLTSIV---NETDFLYNNYTEPTIAPALIAVAPIAQYLAIGKWAAKAFAFSK 57

QY 77 LWGLIFPSGNTLMQDILRETEQFLNQLRNTDTLARVNAELEGLOANREFNQVDNLF- 135
DB 58 VLSLIFPGSQPATMEKVRTEVETLNLQKLSQDRVNILNAEYRG---IEVSDVFDAYIK 113

QY 136 NPTQNPVPLSITSSVNTMQQLFLN-----RLPQFRVQGYQLLLPLFAQAANMHLSEFI 188

Db 114 QPGFPA-----TAKGYFLNLGSAIIQRLQFQEVQYEGVSIALFTQMCTLHLTL 164
QY 189 RDVVLNADEWGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAF-RGLNTRLHDMLEFR 247
Db 165 KDGILAGSAWGTQADVDSFIKLFNQKVDYRTRLMRMYTEEFGRCLKVSLKDGLTFRNM 224
QY 248 MFLNVFEYVSIWLFKYQSLLVSSGANLYASGSPQQTQSFTSQDWPFLYSLFQWNSN-- 305
Db 225 CNLYVFPFAEAWSLMRVEGLKQSSLSL-----WDYVGVGSIPIVNYNEW 267
QY 306 ----YVLNGFSGARLTQTFPNIIGLPGTTTHALLAARVNYSG-----GVSSGDIGAVF 355
Db 268 GGLVYKLLMGEVNRQLTVKFNY----SFTNEPADIPARENIRGVHPYDPSSGLTGWIG 323
QY 356 N---QNFSCSTFLPPLLTPFVRSWLDSGSDRGVNTVTNWQ----- 393
Db 324 NGRTNFNFAD-----NNGNEIMEVTRTQTFYQNPNEPIAPRDIINQILTA 369
QY 394 -----TESFESTL---GLRCGAPTARGN-----SNY--FPDYFIRNI 425
Db 370 PAPADLFFKNADINVKFTQWFQSTLYGWNKLGQTQVLSSRTGTIPPNNLAYDGYIRAI 429
QY 426 SGVPLVVR---NEDLRPLHYNEIRNIESPSG-----TPGGLRAYMVSVHNRKNNIYA 475
Db 430 SACPRGVSLAYNHDL-TTLTYNRI-EYDSPTTENIIVGFAPDNTKDF----YSKKS--- 479
QY 476 VHENGTMHILAPEDYTGFTISPIHATQVNNQTRFISEKFGNQGD-SLRFEQS--NTTAR 532
Db 480 -----HYLSETNDSYVIPALQFAEVSD--RSFLEDTPDQATDGSIKFARTFISNEAK 529
QY 533 YTLRGNGSNLYLRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMG 592
Db 530 YSIRLN-TGFNTATRYKLI---IRVRVPYRL--PAGIRVQSONSGNN-----RMLGSFTA 578
QY 593 NV-----VASDNTNVPLDINV-TFNSGTQFELNMIMFV-----PTNL 628
Db 579 NANPEWVDFVTDFTNDLGTTSSTNALFSISDLSNGEWEYLSQLFLVKESAFTTQI 638
QY 629 PPI 631
Db 639 NPL 641

RESULT 9

C11A_BACTK STANDARD; PRT; 719 AA.
ID C11A_BACTK STANDARD; PRT; 719 AA.
AC Q45752; P71092; Q45750; Q45751; Q45756;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin
DE CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN CRYIIA OR CRYII(A) OR CRYV OR CRYVI OR CGCRYV.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSIR732;
RX MEDLINE=93298009; PubMed=8517758;
RA Gleave A.P., Williams R., Hedges R.J.;
RT "Screening by polymerase chain reaction of Bacillus thuringiensis
RT serotypes for the presence of cryV-like insecticidal protein genes and
RT characterization of a cryV gene cloned from B. thuringiensis subsp.
RT kurstaki";
RL Appl. Environ. Microbiol. 59:1683-1687(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JHCC4835;
RX MEDLINE=92269582; PubMed=1588820;
RA Taitor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;
RT "Identification and characterization of a novel Bacillus thuringiensis

RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";
RL Mol. Microbiol. 6:1211-1217(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=AB88;
RX MEDLINE=96178985; PubMed=8606196;
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
RA Craig J.A., Koziel M.G., Estruch J.J.;
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus
RT thuringiensis: the cryV-encoded protein is expressed early in
RT stationary phase";
RL J. Bacteriol. 178:2141-2144(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=61;
RA Selvapandian A., Bhatnagar R.K.;
RT "Isolation, cloning and expression of cryV gene";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
CC ACTIVE ON PLUTELLA XYLOSTELLA AND BOMBYX MORI.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
CC EMBL; M98544; AAA22354.1; -
DR EMBL; X62821; CAA44633.1; -
DR EMBL; L36338; AAC36999.1; -
DR EMBL; L49391; AAB00958.1; -
DR EMBL; Y08920; CAA70124.1; -
DR PIR; I39815; I39815.
DR PIR; S25383; S25383.
DR HSSP; P02965; ICIV.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
FT VARIANT 159 159 K -> R (IN STRAIN 61).
FT VARIANT 233 233 D -> Y (IN STRAIN JHCC4835 AND HD-1).
FT VARIANT 443 443 A -> V (IN STRAIN AB88).
FT VARIANT 711 712 KQ -> NE (IN STRAIN HD-1 AND 61).
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;
Query Match 9.9%; Score 327.5; DB 1; Length 719;
Best Local Similarity 22.8%; Pred. No. 1.4e-14;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;
QY 21 HDPFSFEHK----SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52

Db 9 HQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSVENVEPVFVSASTIQTGIGIAG 68

QY 53 -IVGTSSFLKKVGLSLGKRIKILSELWGLIFPSPGSTNLMQDILRETEQFLNQLNTDTLA 111

Db 69 KILGTLGVPPFAGQVASY-SFILGELM---PKGK-NQWEIFMEHVEEIIQKISTYARN 122

QY 112 RVNAIEGLQANIREFNQVQVDFNPTQNPVPLSIT-SSVNTMQQLFLNRLPQFRVQGYQ 170

Db 123 KALTDLKGGLDALAVYHDSLSWVGNNRNRARSVVKSQVIALELMFVKLPSPAVSGEE 182

QY 171 LLLLPLFAQAANMHLSEFIRVVLNADWIGISAATLRTYQNYLKNYTTTEYSNYCINTYQTA 230

Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTG 242

QY 231 FRGL-NTRLHDM---EFRTYMLNVFEYVSIWSLFKYQSLLVSSGANL---YASGSGP 282

Db 243 LNNLRGTNAESWVRYNQFRDRLTLMVLDLVALFPSYDQMPYPIKTTAQLTREVTDAIGT 302

QY 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313

Db 303 VHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWGG 362

QY 314 ARLTQTFPNIIGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLTPFV 373

Db 363 HKL--EFRTIGTLNIST-----QGSTNTSINPVTLPFT 394

QY 374 RSWLDGSDRGVNTVT-----NWQ--TESFESTLGLRCGAFARGNSNYFPD 419

Db 395 SRDVYRTESLAGNLFLTPQVNGVRVDFHWKFVTHPIAS-----DNFYYPG 441

QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYA-VHE 478

Db 442 Y-----AGIGTQDSENELPPEATQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494

QY 479 NGTMHILAPEDYTGFTTISPITHATQV-----NNQTRFISEKFG-NQGSRLRPEQSNTTA 531

Db 495 SA-----DRTN-TIENSITQIPLVKAFNLSSGAAVRGPFGFTGGDILR--RTNTGT 543

QY 532 RYTLRGNGN-----SYNLVLRVSSLGNSTIRVTINGRVYVYASNTTNTNNDGVNDNGARF 586

Db 544 FGDIRVINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNR-----GED 596

QY 587 LDINMGVNVASDNTNVPLDINVT-----FNSGTQFELNMIMFVPTNL 628

Db 597 LDYKTRTVGTTPFPFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEV 645

RESULT 10

C1BD_BACTZ STANDARD; PRT; 1231 AA.

AC Q9AZ5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticidal crystal protein cry1Bd (Insecticidal delta-endotoxin

DE Cry1B(d) (Crystalline entomocidal protoxin) (140 kDa crystal protein).

GN Cry1Bd OR Cry1B(D) OR Cry1A1 OR Cry1E1.

OS Bacillus thuringiensis (subsp. wuhanensis).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=52024;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HD-525;

RX MEDLINE=20153386; PubMed=10688690;

RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;

RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.

RT wuhanensis strain."

RL Curr. Microbiol. 40:227-232(2000).

CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLUTELLA

CC XYLOSTELLA.

CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC N-TERMINUS.

CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC -----

DR EMBL; U70726; AAD10292.1; -.

DR HSSP; P02965; 1CIY.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF00555; endotoxin; 1.

DR Pfam; PF03944; endotoxin_C; 1.

DR Pfam; PF03945; endotoxin_N; 1.

KW Toxin; Sporulation.

SQ SEQUENCE 1231 AA; 139654 MW; 129A0371CDDBE52 CRC64;

Query Match 9.9%; Score 327.5; DB 1; Length 1231;

Best Local Similarity 23.3%; Pred. No. 2.9e-14;

Matches 155; Conservative 101; Mismatches 249; Indels 161; Gaps 29;

QY 52 PIVGTSSFLKKVGLSLGKRIKILSELWGLIFPSPGSTNLMQDILRETEQFLNQLNTDTLA 111

Db 73 PFAGQLASFSYFLVG-----ELW---PSG-RDPWEIFLEHVEQLIRQVVTENTRN 118

QY 112 RVNAIEGLQANIREFNQVQVDFNPTQNPVPLSITSSVNTMQQL-FLNRLPQFRVQGYQ 170

Db 119 TAIARLEGLGRYSYQQALETWLDNRDARSILERYVALELDITTAIPLFIRNEE 178

QY 171 LLLLPLFAQAANMHLSEFIRVVLNADWIGISAATLRTYQNYLKNYTTTEYSNYCINTYQTA 230

Db 179 VPLLPIYAQAANLHLLLRDASLFGSEWGMASDDVNYQYQEQIRYTEEYSNHCVQWYNTG 238

QY 231 FRGL-NTRLHDM---EFRTYMLNVFEYVSIWSLFKYQSLLVSSGANL---YASGSGP 282

Db 239 LNNLRGTNAESWVRYNQFRDRLTLMVLDLVALFPSYDQMPYPIKTTAQLTREVTDAIGT 298

QY 283 QQTQ-SFTSQDW-----PFLYSLFQVNSNYV---LNGFSG 313

Db 299 TNAPSGFASTNWFNNNAPSFAIEAAIFRPPHLLDFPEQLTIYSSASSRWSSTQHMNYWVG 358

QY 314 ARLTQTFPNIIGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLTPFV 373

Db 359 HRL--NFRPIGTLNIST-----QGLTNTSINPVTLPFT 391

QY 374 RSWLDGSDRGVNTVT-----WQTESFESTLGLRCGAFARGNSNYFPDYFIRNIS 426

Db 392 SRDVYRTESNAGTNILFTTPVNGVFWARFNFINPQNI-----YERGATTYSQPY-----Q 441

QY 427 GVPLVVRNEDLRPLHYNEIRNIESPS-----GTPGG--LRAYMVS-VH-----467

Db 442 GVGIQFDESETELPPETTERPNVYESYSHRLSHIGLIIGTLRAPVYSWTHRSADRTNTIG 501

QY 468 -NRKNNIYAVHE---NGTMHILAPEDYTGFTTISPITHATQVNNQTRTFISEKFGNQDLSL 522

Db 502 PNRTITQIPAVKGRFLFNGSVI--SGPGFTGGDVVRLNRNNGNIQNRGYI-----EV 550

QY 523 RFEQSNNTARYTLRGNGNSYNLVRVSSLGNSTIRVTI-NGRVYVYASNTTNTNNDGVND 581

Db 551 PIQFTSTSTRYVR-----VRYASVTSIELNVNLGNSSIFTNTLPATAASLDNLQS 601

QY 582 NGARFLDIN-----MGNVVA-----SDNTNVPLD-----INVTNFGTQFEL-----MNI 621

Db 602 GDFGYVEINNAFTSATGNIVGARNFSAEVIIDRFEPFIPVTATFEAEYDLERAQKAVNA 661

QY 622 MFVPTN 627


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Db 662 LFTSTN 667
RESULT 11
CLID_BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin)
DE CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN CRYIID OR CRYI(D) OR NRCRYV.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RX MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
gene.";
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE. ACTIVE ON PLUTELLA
CC XYLOSTELLA AND ON BOMBYX MORI.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF047579; AAD44366.1; --
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
DR Toxin; Sporulation.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
Query Match 9.8%; Score 325; DB 1; Length 719;
Best Local Similarity 22.5%; Pred. No. 2e-14;
Matches 145; Conservative 101; Mismatches 255; Indels 144; Gaps 27;
QY 52 PIVGTVSSFLKKVGLIGKRIKILSELWGLIFPSGSLNMQDILRETEQFLNQLNTDTLA 111
Db 77 PFAGQVAS-----LYSFILGELW---PKGKSQ-WEIFMEHVEELINQKISTYARN 122
QY 112 RVNAELEGLOANTREFNQVDNFL-NPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQ 170
Db 123 KALADLKGGLDALAVYHESLESWIENRNTRVRSVVKQYIALELMFVQKLPFAVSCEE 182
QY 171 LLLLPLFAQAAMHLSFIRDVNLNADEWGISAAATLRTYQNLKNTTTEYSNYCINTYQTA 230
Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSEISITFYNRQSSQTQEYSDYCSEWYNTG 242
QY 231 ---FRGLN---TRLHDMLEFRTYMFNVFEYVSIWSLFKYQSLVSSGAIL- ---YASG 279
Db 243 LNRLRGITNAESWRYN---QFRDMDTLMVLVALFPSPSYDTRMYPITPSAQLTREVYTD 299
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QY 280 SGP-QQTQSFTSQDW-----PFL-----YSLFQVNSN-YVLNG 310
Db 300 IGTVHPNASFASTTWNNAFSTIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 311 FSGARLTQTFPNIGGLPGTTTTHALLAARVNYSGVSSGDIGAVENQNFSCSTFLPPLLT 370
Db 360 WGGHKL--EFTIGTGLNTST-----QGSTNTSINPVTL 391
QY 371 PFVRSWLDGSDRGGVNTVT-----NWQ--TESFESTLGLRCGAPTARGNSNY 416
Db 392 PFTSRDVYRTESLAGLNLFLTPQVNGVPRVDFHWKVFVTHPIAS-----DNFY 438
QY 417 FPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIIYA- 475
Db 439 YPGY-----AGIGTQLODSENELPETTGQPNYESYSHRLSHIG--LISASHVKALVYSW 491
QY 476 VHENGTMHILAPEDYTGFTISPIHATQV-----NNQTRTFISEKFGNQGDSLRFEQSNT 529
Db 492 THRSA-----DRTN-TINSDSITQIPLVKAFNLPASGVVRGPGFTGGDI-LQRTNT 541
QY 530 TARYTLRGNGN-----SYNLYRVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGA 584
Db 542 GTFGDIRVNIINPPFAQRYRLRIRYASTTNLEFHTSINGKAINQGNFSATMNR-GEGLDYK 600
QY 585 RFLDINMGVNVASDNTNVPLDINV-TFNSGTQFELNMIMFVPTNL 628
Db 601 AFRTVGFTTTPFSFNAQSTFTTIGAWNFSGLNEVYIDRIEFVPEV 645
RESULT 12
CLIB_BACTE STANDARD; PRT; 719 AA.
AC Q45709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIIb (Insecticidal delta-endotoxin)
DE CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN CRYIIB OR CRYII(B) OR CRYV OR CRYV465.
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
CC ACTIVE ON PLUTELLA XYLOSTELLA BUT NOT ON BOMBYX MORI.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U07642; AAA82114.1; --
DR PIR; I40590; I40590.
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DR HSP; P02965; 1CIY.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin; 1.
 DR Pfam; PF03944; endotoxin_C; 1.
 DR Pfam; PF03945; endotoxin_N; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

 Query Match 9.4%; Score 310.5; DB 1; Length 719;
 Best Local Similarity 22.7%; Pred. No. 1.9e-13;
 Matches 153; Conservative 116; Mismatches 259; Indels 145; Gaps 34;

 QY 27 EHKS LDTIRKEWMEWKRTDHS LYVA-PIVGT VSSFL LKKVGLSGRIKLS E L WGLIFPSG 85
 Db 47 EHES ID----PFVS ASTIQTGIGIAGKILGT LGVPFAGQIASLY-SFILGELW----PKG 97

 QY 86 STNL MQDILRETEQFLNORLNTDTLARVNAELEG LQANIREFNNQVDN FLNPTQNVPVLS 145
 Db 98 KSQ-WEIFMEHVEEIIINQILTYARNKALSD LRG L GDALAVYHESLESWVENRNNTRARS 156

 QY 146 IT-SSVNTMQQLFLNRLPQFRVQGYQLLLLPLFQAQANMHL SFIRDVVLNADEWGISAA T 204
 Db 157 VVKNQYIALELMFVQKLESFVSGEEVPLLP IYQAQANLHLLLRDASIFGKEWGLSASE 216

 QY 205 LRTYQNYLKNYTT EYSNYCINTYQTA---FRGLNTRLHDML-EFRTYMF LNVFEYVS IWS 260
 Db 217 ISTFYNRQVERTRDYS DHC I KWYNTGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFP 276

 QY 261 LFKYQSL L--VSSGANL-----YASGSGP-QQTQSFTSQDWPFLYSLFQVNSNYVLNGFSG 313
 Db 277 --SYDTLVYPIKTTSQLTREVVYTDAGTVHPNQAFAS TTW-----YNNNAPSFS AIE 326

 QY 314 ARLTQTFPNIGGLPGTTTHALLA-----ARVNYSGG-VSSGDIGAVFNQNFSCSTFLP 366
 Db 327 AAVIRS-PHLLDFLEKVTIYSLLSRWSNTQYMMWGGHLESRPIGGALNT----- 376

 QY 367 PLLTFFVRSWLDGSGDRGGVNTVTNWQTESF-----ESTLGLRCGAFTARGNSNYFP 418
 Db 377 -----STQGSTNTSINPVTLOFTSRDVYRTESLAGLNL----- 409

 QY 419 DYFIRNISGVP-----LVVRNEDLRRPLHY-----NEIRNIES--PSGTPG-- 457
 Db 410 -FLTQPVNGVPRVDFHWKFPPTLP IASDN----FYVLGYAGVGTQLQDSENELPPE TTGQP 464

 QY 458 GLRAY-----MVSVHNKRKN IYA-VHENG TMHLAPEDYTGFTISPIHATQV----- 503
 Db 465 NYESYSHRLSHIGLISASHVKALVYSWTHRSA-----DRTN-TIEPNSITQIPLVKA 515

 QY 504 -NNQTRTFISEKFG-NQGD SLRFEQSNTTARYTLRNGN-----SYNLYLRVSSLGNSTI 556
 Db 516 FNLSSGA AVVRGPGFTGGDILR--RTNTGTFGDIRVNNPFPFAQRYRVRIRYASTTDLQF 573

 QY 557 RVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDNTNVPLDINV-TFNSGTQ 615
 Db 574 HTSINGKAINQGNFSATMNR-GEDLDYKTFRTIGFTTFFSFSDVQSTFTIGAWNFSGNE 632

 QY 616 FELMNMIFVPTNL 628
 Db 633 VYIDRIEFVPEV 645

CRY9CA OR CRYIXC(A).
Bacillus thuringiensis (subsp. tolworthi).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1442;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=BTS02618A;
MEDLINE=96141404; PubMed=8572715;
Lambert B., Buysse L., Decock C., Jansens S., Piens C., Saey B.,
Seurinck J., Van Audenhove K., Van Rie J., Van Vliet A., Peferoen M.;
"A Bacillus thuringiensis insecticidal crystal protein with a high
activity against members of the family Noctuidae.";
Appl. Environ. Microbiol. 62:80-86(1996).
-!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD
SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,
PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST
INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO
ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO
BEETLE.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
THE SPORE COAT.
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
TERMINUS.
-!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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EMBL; Z37527; CAA85764.1; -.
PIR; A59350; S49247.
HSP; P07130; 1DLC.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
Pfam; PF00555; endotoxin; 1.
Pfam; PF03944; endotoxin_C; 1.
Pfam; PF03945; endotoxin_N; 1.
Toxin; Sporulation.
SEQUENCE 1157 AA; 129775 MW; C364391EF7FDFB8A CRC64;



Db 359 RFPVSSNF-MDYWSGHTLRRSYLNDLSAVQEDSYGLITTTTRATINPGVDGTNRIESTAVDF 417
QY 353 -----AVFNQNFESCSTFLPPLTTPFVRSWLDGSD---RGGVNTV--TNWQTESFESTLG 402
Db 418 RSALIGIYGVN-----RASFPVGGFLNGTTSPPANGGCRDLDTNDELPPDEST-- 465
QY 403 LRCGAFTARGNSYFPDY-----FIRNISGVPLVV---RNEDLRRPLHYNEIRNIESPS 453
Db 466 ---GSSTHRLSHVTFSSFTNQAGSIANAGSVPTVWTRRDVDLNNITPNNRITQLP--- 519
QY 454 GTPGGLRAYMVSVHNRKNNIYAVHENGTMTHLAPEDYTGFTISPIHATQVNNQTRTFISE 513
Db 520 -----LVKA-----SAPVSGTTVLKGP-----GFT----- 539
QY 514 KFGNQDLSLRFQOSNTTARYTLRGNNS-----YNLYLRVSSLGNSTIRVTIN---GRV 564
Db 540 ---GGILRRRTNGTFG--TLRVTVNSPLTQQYRLRVRFASFGNFSIRVLRGVSGIDV 593
QY 565 YTASNVN-----TTT-----NNDGVNDNGARFLD--- 588
Db 594 RLGSTMRGQELTYESFFTRFTTTGPNFPFTTQAEILTVNAEGVSTGGEYIDRIE 653
QY 589 ---INMGNVVASD-----NTNVPLDINVT 609
Db 654 IVPVNPAREAEEDLEAAKAVASLFTTRTRDGLQNVNT 690

RESULT 14
C7AB BACUA STANDARD; PRT; 1138 AA.
AC Q45707;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticialidal crystal protein cry7Ab (Insecticidal delta-endotoxin
DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN CRY7AB OR CRYVIIA(B).
OS Bacillus thuringiensis (subsp. dakota).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD511;
RA Payne J.M., Fu J.M.;
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins."
RL Patent number US5286486, 15-FEB-1994.
CC -I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -I- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -I- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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or send an email to license@isb-sib.ch).

EMBL; U04367; AAA21120.1; -
DR HSSP; P07130; 1DLCL.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.

KW Toxin; Sporulation.
SQ SEQUENCE 1138 AA; 129778 MW; 01DF7072C074CE88 CRC64;
Query Match 9.2%; Score 306; DB 1; Length 1138;
Best Local Similarity 20.0%; Pred. No. 7.3e-13;
Matches 135; Conservative 109; Mismatches 222; Indels 208; Gaps 25;
QY 52 PIVGTSSFLKKVGLIGRIKRIISLWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLA 111
Db 76 PGASFITNFKL-----ITGLWPH-NKNIWDEFMTEVETLIEQKIEQYARN 121
QY 112 RVNALEGLQANIREFNQVDNFINPTQNPVPLS-ITSSVNTMQQLFLNRLPQFRVQGYQ 170
Db 122 KALAELEGLGNLTIIYQQALEDWLNPPDDPATITRVIDRFRILDALFESYMPFRVAGYE 181
QY 171 LLLLPLFAQAAMHLSFIRDVVLNADEWGISAAATLRTYQNVLYKNYTTTEYSNYCINTYQTA 230
Db 182 IPLLTVYAQAANLHALLRDLSTLYGDKWGFTQNNIEENYNRQKKHISEYSNHCVKWYNSG 241
QY 231 FRGLNTRLHMDL---EFRTYMFNLNVEYVSIWLSFKYQSLLVSSGANLYASGGPQQTQ 286
Db 242 LSRLNGSTYEQWINYNRRFRREMILMVLIDIAAVFPIYD----- 278
QY 287 SFTSQDWPFYLSLFQVNSYVNLGPFSGARLTQTTPNIGGLPGTTTHALLAARVNYSGV 346
Db 279 -----PRMYSM-----ET-----STQLTREVVYTDPISL--I 303
QY 347 SSGDIGAVFNQNFSCSTFLPPLTTPFVRSWLD----- 378
Db 304 SNPDIGPFSQMENTA-----FRTPHLVDYLDDELYIYTSKYKAFSHEIQDPLFYWCVKV 358
QY 379 --SGDRGGVNTVTNWQTESFESTLG-LRCGAFTARGNSNYFPDYFIRNISGVPLVVRNE 435
Db 359 SFKSEQSNLYT---TGIYGKTSGYISSGAYSFRGNDIY-----RTLAAPSVVV--- 404
QY 436 DLRRPLHYNEIRNIESPS--GTPGGLRAYMVSVHNRKNNIY-----AVHE 478
Db 405 -----YPTQNYGVEQVEFYGVKG-----HVHYRGDNKYDLYTDSIDQLPPDGEPIHE 452
QY 479 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNNTA 531
Db 453 KYTHRLCHATAISKSTPDYDNATI-PFSW-----THRSAEYNYRIYPNKIKIPAVK 504
QY 532 RYTL-----RG-NG-----NSYNLYLRVSSLGNSTIR 557
Db 505 MYKLDLSTVVKGPGFTGGDLVKRGSNGYIGDIKATVNSPLSQYRVVRVYATSVSGLFN 564
QY 558 VTINGRVYTASNVT--TNNDGVNDNGARFLDINMGNVVASDNTNVPLDINVT-FNSGT 614
Db 565 VFINDETALQKNFQSTVETIGEGKDLTYGSFGYIEYSTTIQFPNEHPKITLHLNHLNNS 624
QY 615 QFELMNIMFVPTNL 628
Db 625 PFYVDSIEFIPVDV 638

RESULT 15
CIBE_BACTU STANDARD; PRT; 1227 AA.
ID CIBE_BACTU
AC O85805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticialidal crystal protein cryIbe (Insecticidal delta-endotoxin
DE CryIB(e)) (Crystalline entomocidal protoxin) (139 kDa crystal protein).
GN CRYIBE OR CRYIBE(E) OR 158C2B.
OS Bacillus thuringiensis.
OG Plasmid pMYC2383.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-18872 / PS158C2;

RA Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
RT "Bacillus thuringiensis genes encoding lepidopteran-active toxins."
RL Patent number US5723758, 03-MAR-1998.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF077326; AAC32850.1; -;
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation; Plaemid.
SQ SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;

Query Match 9.2%; Score 305.5; DB 1; Length 1227;
Best Local Similarity 22.5%; Pred. No. 8.8e-13;
Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;
QY 52 PIVGTVSSFLKKVGLIGKRILSELWGLIFPSGSTNLMQDILRETEQFLNQRINTDTLA 111
DB 73 PFAGQIASFYSLVG-----ELW---PRG-RDPWEIFLEHVEQLIRQQVTENTRD 118
QY 112 RVNAELEGLOANIREFNQVDNFLNPTQNPVPLSITSSVNTMQQL-FLNRLPQFRVQYQ 170
DB 119 TALARLQGLGNSFRAYQOSLELDWLENRDDARTSRVLYTQYIALELDFLNAMPFLFAIRNOE 178
QY 171 LLLLPLFAQAAMHLSFIRDVVLNADEWGISATLRTYQNLKNTTEYSNYCINTYQTA 230
DB 179 VPLLVMVYAQAANLHLLLRDASLFGSEFGLTSQBIQRYERYQVEKTRREYSDYCARWYNTG 238
QY 231 FRGL-NTRLHML--EFRTYMLNVFEYVSIWLFKYQSLLVSSGANL---YASGSGP 282
DB 239 LNNLRGTNAESWLRYNQFRDRLTLGLVDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGR 298
QY 283 QQTQS-FTSQDWPFYLSLFQVNSNYVLNGFSGARLTQTF-PNIGGLPGTTTHALLAARV 340
DB 299 TNAPSGFASTNW-----FNNN--APSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWS 348
QY 341 NYSGGVSSGDIGAVFNQNFSCSTFLPPLLTPFVRSW----LDGSDRGVNTVTN----- 391
DB 349 N-----TQYMYVWVGHRLSRTIRGSLSTSTHGNTNT 380
QY 392 -----WQTESFES-----TLGLRCGAFTARGNSNYFPDYFIRNI--SG 427
DB 381 SINPVTLQTSRDVYRTESFAGINILLTTPVNGVPWARFNWRNPLNSLRGSLLYTIGYTG 440
QY 428 VPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYA-VHENGTMHLA 486
DB 441 VGTQLFDSETELPPEPTEPPEPTEPPEPTEPPEPTEPPEPTEPPEPTEPPEPTEPPEPTE 492
QY 487 PEDYTGFTISPIHATQVN-----NQRTTFISEKFGNQDLSLRFQSNITARYTLRGNG 539
DB 493 --DRTN-TISSDSITQIPLVKSFNLNSGTSVSGPGFTGGDIIRTNVNGSVLSMGLNFNN 549
QY 540 NS---YNLYLRVSSLGNSTIRVTING-RVYTASNVTNTTNDGVDNDNGARFLDINMGNVV 595

Db 550 TSLQRYRVRYAASQTMVLRVTVGSTTFDQGFPSMTSANEESLTQSFRFAEFPVVGISA 609
QY 596 ASDNTNVPLDINVTFNSGTQ-FELMNMIMFVP 625
Db 610 SGSQT---AGISISNNAGRQTFHFEDKIEFIP 637
Search completed: December 12, 2003, 16:16:44
Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 16:14:45 ; Search time 21 Seconds
(without alignments)
2894.219 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
Sequence: 1 MNVNLNGRTTICDAYNVVA.....GTQFELMNIMFVPTNLPPIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3048.5	92.0	633	2 C32053	parasporal crystal
2	3010.5	90.8	633	2 D32053	parasporal crystal
3	2545	76.8	622	2 S17402	parasporal crystal
4	336.5	10.2	643	2 A43647	parasporal crystal
5	327.5	9.9	719	2 I39815	insecticidal prote
6	324.5	9.8	719	2 S25383	parasporal crystal
7	324.5	9.8	719	2 I39814	insecticidal prote
8	310.5	9.4	719	2 I40590	cryV465 protein -
9	307	9.3	1157	1 S49247	parasporal crystal
10	294.5	8.9	1176	2 A48970	parasporal crystal
11	282.5	8.5	1176	2 JT0241	parasporal crystal
12	280.5	8.5	934	2 A22798	parasporal crystal
13	277.5	8.4	380	2 B42459	hypothetical prote
14	277	8.4	1181	2 A41052	parasporal crystal
15	276.5	8.3	1176	2 JC2219	parasporal crystal
16	275.5	8.3	1228	2 S00873	parasporal crystal
17	273	8.2	1155	2 A26513	parasporal crystal
18	271.5	8.2	1176	2 A22617	parasporal crystal
19	271.5	8.2	1176	2 S02215	parasporal crystal
20	269	8.1	1155	2 S02134	parasporal crystal
21	268	8.1	1155	2 JD0002	parasporal crystal
22	268	8.1	1156	2 A29125	parasporal crystal
23	267.5	8.1	1178	1 USBSXH	parasporal crystal
24	267	8.1	1155	2 I39838	parasporal crystal
25	265	8.0	1174	2 A42459	parasporal crystal
26	264.5	8.0	1160	2 I40589	parasporal crystal
27	264	8.0	1174	2 S32649	parasporal crystal
28	262.5	7.9	1156	2 A29838	parasporal crystal
29	261.5	7.9	1172	2 S32689	parasporal crystal

30	259	7.8	1165	2 S11446	parasporal crystal
31	259	7.8	1177	2 A49785	parasporal crystal
32	255.5	7.7	649	1 JH0261	parasporal crystal
33	253	7.6	618	2 S11445	parasporal crystal
34	253	7.6	1138	2 A48944	parasporal crystal
35	250	7.5	652	2 A27323	parasporal crystal
36	249.5	7.5	652	2 I39811	parasporal crystal
37	247.5	7.5	659	2 S10228	parasporal crystal
38	244	7.4	1160	2 S32647	parasporal crystal
39	237	7.2	613	2 JC6033	parasporal crystal
40	230.5	7.0	655	2 JC7140	mosquitocidal prot
41	229.5	6.9	1189	2 S00944	protoxin - Bacillu
42	225	6.8	823	2 S04181	parasporal crystal
43	218.5	6.6	1171	2 A37829	parasporal crystal
44	218.5	6.6	1171	2 I40572	parasporal crystal
45	216	6.5	1154	2 S39536	parasporal crystal

ALIGNMENTS

RESULT 1

C32053

parasporal crystal protein B1 - Bacillus thuringiensis subsp. kurstaki

N;Alternate names: parasporal crystal protein P2

C;Species: Bacillus thuringiensis subsp. kurstaki

C;Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 15-Oct-1999

C;Accession: C32053; A29913

R;Widner, W.R.; Whiteley, H.R.

J. Bacteriol. 171, 965-974, 1989

A;Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subs

A;Reference number: A32053; MUID:89123178; PMID:2914879

A;Accession: C32053

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-633 <WID>

R;Donovan, W.P.; Dankocsik, C.C.; Gilbert, M.P.; Gawron-Burke, M.C.; Groat, R.G.; Carlot

J. Biol. Chem. 263, 561-567, 1988

A;Title: Amino acid sequence and entomocidal activity of the P2 crystal protein. An inse

A;Reference number: A29913; MUID:88087146; PMID:3121615

A;Accession: A29913

A;Molecule type: DNA

A;Residues: 1-587, 'FRY' <DON>

C;Genetics:

A;Gene: cryBI

Query Match 92.0%; Score 3048.5; DB 2; Length 633;
Best Local Similarity 90.7%; Pred. No. 6.7e-200;
Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

Qy	1	MNVNLNGRTTICDAYNVVAHDPFSFEHKSLDTIRKEWMWKRTDHSLYVAPIVGTVSSP	60
Db	1	MNVNLNGRTTICDAYNVVAHDPFSFEHKSLDTIQKEWMWKRTDHSLYVAPIVGTVSSP	60
Qy	61	LLKKVGSGLIGKRIISELWGLIFPSSGSTNLMQDILRETEQFLNQLRTDTLARVNAEGL	120
Db	61	LLKKVGSGLIGKRIISELWGLIFPSSGSTNLMQDILRETEQFLNQLRTDTLARVNAELIGL	120
Qy	121	QANIREFNQQVDNLFNPTQNVPPLSITSSVNTMQQLFNLRLPQFRVQGYQLLLPLFAQA	180
Db	121	QANIREFNQQVDNLFNPTQNVPPLSITSSVNTMQQLFNLRLPQFIQGYQLLLPLFAQA	180
Qy	181	ANMHLFIRDVVLNADWIGISAATLRTYQNYLKNYTTSEYSNYCINTYQTAFGLNTRLHD	240
Db	181	ANMHLFIRDVILNADWIGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFGLNTRLHD	240
Qy	241	MLEFRTYMFLNVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYSLF	300
Db	241	MLEFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANLYASGSGPQQTQSFTAQWPFYSLF	300
Qy	301	QVNSNYVLNFGSGARLTQTFFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAV-FNQNF	359
Db	301	QVNSNYILSGISGTRLSITFPNIGGLPGSTTTHSLNSARVNYSGGVSSGLIGATNLNHNH	360

QY	360	SCSTFLPPLLT	PFVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAF	TARGNSNYFPD	4119
Db	361	NCSTVLPLST	PFVRSWLDSGTREGVATSTNWQTESFQTTLSLRCGAFS	ARGNSNYFPD	420
QY	420	YFIRNISGVPL	VRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVS	VHNRKNNIYAVHEN	479
Db	421	YFIRNISGVPL	VRNEDLTRPLHYNQIRNIESPSGTPGGARAYLVS	VHNRKNNIYAANEN	480
QY	480	GTMIHLAPEDY	TGFTISPIHATQVNNQTRTFISEKFGNQGDSLRF	EQSNTTARYTLRGNG	539
Db	481	GTMIHLAPEDY	TGFTISPIHATQVNNQTRTFISEKFGNQGDSLRF	EQSNTTARYTLRGNG	540
QY	540	NSYNLYLRVSSL	GNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLD	INMGNVVASDN	599
Db	541	NSYNLYLRVSS	IGNSTIRVTINGRVYTVSNVNTTNTNDGVNDNGARFSD	INIGNIVASDN	600
QY	600	TNVPLDINVT	NSGTQFELMNI	MFVPTNLPIY	632
Db	601	TNVPLDINVT	LSGTPFDLMNI	MFVPTNLPLY	633

RESULT 2

D32053
parasporal crystal protein B2 - *Bacillus thuringiensis* subsp. *kurstaki*
C/Species: *Bacillus thuringiensis* subsp. *kurstaki*
C/Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 15-Oct-1999
C/Accession: D32053; S12396
R/Widner, W.R.; Whiteley, H.R.
J. Bacteriol. 171, 965-974, 1989
A/Title: Two highly related insecticidal crystal proteins of *Bacillus thuringiensis* subsp. *kurstaki*
A/Reference number: A32053; MUID:89123178; PMID:2914879
A/Accession: D32053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-633 <WID>
R/Dankocsik, C.; Donovan, W.P.; Jany, C.S.
Mol. Microbiol. 4, 2087-2094, 1990
A/Title: Activation of a cryptic crystal protein gene of *Bacillus thuringiensis* subsp. *kurstaki*
A/Reference number: S12396; MUID:91211618; PMID:2089222
A/Accession: S12396
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-633 <DAN>
A/Cross-references: EMBL:X55416; NID:q40311; PIDN:CAA39075.1; PID:q40312

RESULT 3

S17402
parasporal crystal protein cry2Acl - Bacillus thuringiensis plasmid
N;Alternate names: delta-endotoxin; parasporal crystal protein cryIIC
C;Species: Bacillus thuringiensis
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S17402
R;Wu, D.; Cao, X.L.; Bai, Y.Y.; Aronson, A.I.
FEMS Microbiol. Lett. 81, 31-36, 1991
A;Title: Sequence of an operon containing a novel delta-endotoxin gene from Bacillus thuringiensis
A;Reference number: S17400
A;Accession: S17402
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-622 <WUD>
A;Cross-references: EMBL:X57252; NID:G40283; PIDN:CAA40536.1; PID:G40286
C;Genetics:
A;Genome: plasmid
C;Keywords: delta-endotoxin

Query Match 76.8%; Score 2545; DB 2; Length 622;
Best Local Similarity 78.9%; Pred. No. 1.3e-165;
Matches 501; Conservative 45; Mismatches 73; Indels 16; Gaps 8;



QY 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313
Db 303 VHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNWGG 362
QY 314 ARLTQTFFNIGGLPGTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLTPFV 373
Db 363 HKL--EFTIGGTLNIST-----QGSTNTSINPVTLPFT 394
QY 374 RSWLDGSDRGVNTVT-----NWQ--TESFESTLGLRCGAFTARGNSNYFPD 419
Db 395 SRDVYRTESLAGNLFLTQPVNGVPRVDFHWKFVTHPIAS-----DNFYYPG 441
QY 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYA-VHE 478
Db 442 Y-----AGIGTQLQDSENELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494
QY 479 NGTMIHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NQGDLSLRFESQNTTA 531
Db 495 SA-----DRTN-TIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILR--RTNTGT 543
QY 532 RYTLRGNGN-----SYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARF 586
Db 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
QY 587 LDINMGNVVASDNTNVPLDINVT-----FNSGTQFELMNMIMFVPTNL 628
Db 597 LDYKTRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEV 645

RESULT 6

S25383
parasporal crystal protein cryIIa1 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin; parasporal crystal protein cryv
C;Species: Bacillus thuringiensis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 01-Dec-2000
C;Accession: S25383
R;Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A;Reference number: S25383; MUID:92269582; PMID:1588820
A;Accession: S25383
A;Molecule type: DNA
A;Residues: 1-719 <TAI>
C;Genetics:
A;Gene: cryv
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 9.8%; Score 324.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 3.5e-14;
Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;

QY 21 HDPFSFEHK-----SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPVSASTIQTGIGIAG 68
QY 53 -IVGTVSSFLKKVGLIGKRILSELWGLIFPSPGSTNLMQDILRETEQFLNRLNTDTLA 111
Db 69 KILGTGVFPFAGQVASLY-SFILGELW---PKGK-NQWEIFMEHVEEIIINQKISTYARN 122
QY 112 RVNAELEGLOANIREFNQVDNFLNPTQNPVPLSIT--SSVNTMQQLFLNRLPQFRVQGYQ 170
Db 123 KALTDLKGLDALAVYHDSLESWVGVRNNTARSVVKSQYIALELMFVQKLPFAVSCEE 182
QY 171 LLLLPLFAQAANMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTTTEYSNYCINTYQTA 230
Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMYSTG 242
QY 231 FRGL-NTRLHDM-----EFRTYMFNLNVEYVSIWSLEFKYQSLLVSSGANL-----YASGSGP 282
Db 243 LNNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGT 302

QY 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313
Db 303 VHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNWGG 362
QY 314 ARLTQTFFNIGGLPGTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLTPFV 373
Db 363 HKL--EFTIGGTLNIST-----QGSTNTSINPVTLPFT 394
QY 374 RSWLDGSDRGVNTVT-----NWQ--TESFESTLGLRCGAFTARGNSNYFPD 419
Db 395 SRDVYRTESLAGNLFLTQPVNGVPRVDFHWKFVTHPIAS-----DNFYYPG 441
QY 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYA-VHE 478
Db 442 Y-----AGIGTQLQDSENELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494
QY 479 NGTMIHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NQGDLSLRFESQNTTA 531
Db 495 SA-----DRTN-TIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILR--RTNTGT 543
QY 532 RYTLRGNGN-----SYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARF 586
Db 544 FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
QY 587 LDINMGNVVASDNTNVPLDINVT-----FNSGTQFELMNMIMFVPTNL 628
Db 597 LDYKTRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEV 645

RESULT 7

I39814
insecticidal protein cryVI - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: I39814
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:953114293; PMID:7793960
A;Accession: I39814
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: GB:L36338; NID:g540281; PIDN:AAC36999.1; PID:g540282
C;Genetics:
A;Gene: cryVI
C;Superfamily: parasporal crystal protein

Query Match 9.8%; Score 324.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 3.5e-14;
Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;

QY 21 HDPFSFEHK-----SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPVSASTIQTGIGIAG 68
QY 53 -IVGTVSSFLKKVGLIGKRILSELWGLIFPSPGSTNLMQDILRETEQFLNRLNTDTLA 111
Db 69 KILGTGVFPFAGQVASLY-SFILGELW---PKGK-NQWEIFMEHVEEIIINQKISTYARN 122
QY 112 RVNAELEGLOANIREFNQVDNFLNPTQNPVPLSIT--SSVNTMQQLFLNRLPQFRVQGYQ 170
Db 123 KALTDLKGLDALAVYHDSLESWVGVRNNTARSVVKSQYIALELMFVQKLPFAVSCEE 182
QY 171 LLLLPLFAQAANMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTTTEYSNYCINTYQTA 230
Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMYSTG 242
QY 231 FRGL-NTRLHDM-----EFRTYMFNLNVEYVSIWSLEFKYQSLLVSSGANL-----YASGSGP 282
Db 243 LNNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYDAIGT 302



QY 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSG 313
Db 303 VHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGG 362
QY 314 ARLTQTFNIGGLPGTTTTHALLAARVNYSGGVSSGDIGAVNQNFSCSTFLPPLLPFV 373
Db 363 HKL--EFRTIGTLNIST-----QGSTNTSINPVTILPFT 394
QY 374 RSWLDSGSDRGVNTVT-----NWQ--TESFESTGLRCGAFARGNSNYPPD 419
Db 395 SRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIAS-----DNFYYPG 441
QY 420 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYA-VHE 478
Db 442 Y-----AGIGTQLQDSENELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494
QY 479 NGTMIHLAPEDYTGTTISPIHATQV-----NNQTRTFISEKFG-NQGDLSRFEQSNTTA 531
Db 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNLTGT 543
QY 532 RYTLRGNGN-----SYNLYL RVSSLSGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARF 586
Db 544 FGDIRVNINPPFAQRYRVRIRVASTTDLOFHTSINGKAINQGNFSATMNR-----GED 596
QY 587 LDINMGVNASDNTNVPLDINVT-----FNSGTQFELNMIMFVPTNL 628
Db 597 LDYKTRTVGFTTTPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEV 645

RESULT 8
I40590
cryV465 protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999
C;Accession: I40590
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I40590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-719 <RES>
A;Cross-references: EMBL:U07642; NID:G467234; PIDN:AAA82114.1; PID:G467235
C;Genetics:
A;Gene: cryV465
C;Superfamily: parasporal crystal protein

Query Match 9.4%; Score 310.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 3.1e-13;
Matches 153; Conservative 116; Mismatches 259; Indels 145; Gaps 34;
QY 27 EHKSLDTIRKEWMEWKRTDHSLYVA-PIVGTVSSFLKKVGSLLIGKRILSELWGLIPPSG 85
Db 47 EHESID----PFVSASTIQTGIGIAGKILGTGVPFAGQIASLY-SFILGELW----PKG 97
QY 86 STNLMQDILRETEQFLNORLNTDTLARVNAELEGLOANIREFNQQVDNFLNPTQNVPVLS 145
Db 98 KSQ-WEIFMEHVEEIIQKILTYARNKALSDRLGLDALAVYHESLESWVENRNNTRARS 156
QY 146 IT-SSVNTMQQLFLNRLPQFRVQYQLLLPLFAQAANMHLSFIRDVVLNADEWGISAAAT 204
Db 157 VVKQNYIALELMFVQKLPFSAVSGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASE 216
QY 205 LRTYQNYLKNYTTESNYCINTYQTA---FRGLNTRLHMDL-EFRTYMFLNVFEYYSIWS 260
Db 217 ISTFYNRQVERTRDYSDDHCKIKNYNTGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFP 276
QY 261 LFKYQSL--VSSGANL----YASGSGP-QQTQFTSQDWPFLYSLFQVNSNYVLNGFSG 313
Db 277 --SYDTLVYPIKTTSQLTREVTYDAIGTVHPNQAFASFTW-----YNNNAPSFAIE 326

QY 314 ARLTQTFNIGGLPGTTTTHALLA-----ARVNYSGG--VSSGDIGAVNQNFSCSTFLP 366
Db 327 AAVIRS-PHLLDFLEKVTIYSLLSRWSNTQYMMWGGHRLSRPIGGALNT----- 376
QY 367 PLLTPFVRSWLDSGSDRGVNTVTNWQTESF-----ESTGLRCGAFARGNSNYFP 418
Db 377 -----STQGSTNTSINPVTLOFTSRDVYRTESLAGLNL----- 409
QY 419 DYFIRNISGVP-----LVVRNEDLRRPLHY-----NEIRNIES--PSGTPG-- 457
Db 410 -FLTQPVNGVPRVDFHWKFPTLPIASDN----FYLYGAGVGTQLQDSENELPPEQTGP 464
QY 458 GLRAY-----MVSVHNRKNNIYA-VHENGTMHILAPEDYTGTTISPIHATQV----- 503
Db 465 NYESYSHRLSHIGLISASHVKALVYSWTHRSA-----DRTN-TIEPNSITQIPLVKA 515
QY 504 -NNQTRTFISEKFG-NQGDLSRFEQSNTTARTYTLRGNGN-----SYNLYL RVSSLSGNSTI 556
Db 516 FNLSSGAAVVRGPGFTGGDILR--RTNTGTGFDIRVNINPPFAQRYRVRIRVASTTDLOF 573
QY 557 RVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGVNASDNTNVPLDINV-TFNSGTQ 615
Db 574 HTSINGKAINQGNFSATMNR-GEGLDYKTFRTIGTTPFSFSDVQSTFTIGAWNFSSGNE 632
QY 616 FELNMIMFVPTNL 628
Db 633 VYIDRIEFVPEV 645

RESULT 9
S49247
parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIh
C;Species: Bacillus thuringiensis
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: A59350; S49247
R;Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; v
Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agai
A;Reference number: A59350; MUID:96141404; PMID:8572715
A;Accession: A59350
A;Molecule type: DNA
A;Residues: 1-1157 <LAM>
A;Cross-references: EMBL:Z37527; NID:G547554; PIDN:CAA85764.1; PID:G547556
A;Experimental source: serovar tolworthi
C;Comment: This parasporal crystal protein, active against corn borer and other insects,
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 9.3%; Score 307; DB 1; Length 1157;
Best Local Similarity 23.4%; Pred. No. 1.1e-12;
Matches 163; Conservative 87; Mismatches 215; Indels 232; Gaps 34;
QY 52 PIVGTVSSFLKKVGSLLIGKRILSELWGLIPPSGSTNLMDILRETEQFLNORLNTDTLA 111
Db 87 PFSGQIVSFY-----QFLNLTLW----PVNDTAIWEAFMRQVEELVNOQITEFARN 133
QY 112 RVNAELEGLOANIREFNQQVDNFL--NPTQNPVPLSITSSVNTMQQL-FLNRLPQFRVQ 167
Db 134 QALARLOGLGDSFNVYQRSLONLWADRNDFTN---LSVVRAQFIALDLDFVNAIPLFAVN 190
QY 168 GYQLLLLPLFAQAANMHLSFIRDVVLNADEWGISAAATLRTYQNYLKNYTTESNYCINTY 227
Db 191 GQQVPLLSVYAQAVNLHLLLLKDSALFGEWGFTQGEISTYYDRQLELTAKYTNYCETWY 250
QY 228 QTA---FRGLNT----RLHDMLEFRTYMFLNVFEYYSIWSLFKYQSLLVSSGANLYASGS 280
Db 251 NTGLDRLRGTTNTESWLYRH---QFRREMTLVVLDVW---ALFPYYDV-----RLYPTGS 298
QY 281 GPQQTQS-FTS-----QDW-----PFLY-----S 298
Db 299 NPQLTREVTYDPIVFNPPANVGLCRRWGNTPNYTFSELENAFIRPPHLPDRLNSLTISSN 358

QY	299	LFQVNSNYVLNGFSGARLTQTFFPNIGGLPG-----TTTTHALLAARVMYSGGVSSGDIG-	352
Db	359	RFPVSSNF-MDYWSGHTLRRSYLNDSAVQEDSYGLITTTTRATINPGVDGTRNRIESTAVDF	417
QY	353	-----AVFNQNFSCSTFLPPLLTFFVRSWLDSGSD--RGGVNTV--TNWQTESFESTLG	402
Db	418	RSALIGIYGVN-----RASFPVPGFLFNGTTSPANGGCCRDLYDINDELPPDEST--	465
QY	403	LRCGAPTARGNSYFPDY-----FIRNISGVPLVW--RNEDLRRPLHYNEIRNIESPS	453
Db	466	---GSSTHRLSHVTFFSFQTNQAGSIANAGSVPTYVWTRRRDVLNNTITPNRITQLP---	519
QY	454	GTPGGLRAYMVSVHNRKNNIYAVHENGMTMIHLAPEDYTGFTISPIHATQVNNQTRTFISE	513
Db	520	-----LVKA-----SAPVSGTIVLKGp-----GFT-----	539
QY	514	KFGNQGDSLRFEQSNTTARYTLRGNGNS-----YNLYLRVSSLGNSTIRVTIN---GRV	564
Db	540	---GGGILRRTTNGTFG--TLRVTVNSPLTQQYRLRVRFASGTGNFSIRVLRGGVSIGDV	593
QY	565	YTASNVN-----TTT-----NNDGVNDNGARFLD---	588
Db	594	RLGSTMNRGQELTYESFFTRFTTTGPFNPFPFTTQAOEILTVNAEGSVSTGGEYYIDRIE	653
QY	589	---INMGNVVVASD-----NTNVPLDINVT	609
Db	654	IVPVPAREAEEDLEAAKKAVASLFTFRDGLQVNV	690

RESULT 10

parasporal crystal protein crylCb - *Bacillus thuringiensis*
C/Species: *Bacillus thuringiensis*
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C/Accession: A48970
R;Kalman, S.; Kiehne, K.L.; Libs, J.L.; Yamamoto, T.
Appl. Environ. Microbiol. 59, 1131-1137, 1993
A/Title: Cloning of a novel cryIC-type gene from a strain of *Bacillus thuringiensis* subs
A/Reference number: A48970; MUID:93236401; PMID:8476286.
A/Accession: A48970
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-1176 <KAL>
A/Cross-references: GB:M97880; NID:g289263
A/Experimental source: subsp. galleriae HD29
A/Note: sequence extracted from NCBI backbone (NCBIN:129672, NCBIPI:129675)
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match	8.9%;	Score 294.5;	DB 2;	Length 1176;
Best Local Similarity	22.6%;	Pred. No. 7.9e-12;		
Matches 160;	Conservative 110;	Mismatches 246;	Indels 191;	Gaps 38;

QY	2	NNVLNNGRTTICDAYNVVAH-----DPFSFEHKSLDITIRKEWMEWKRTDHSLSYVAPI	53
DB	3	NNIQNQ-----CVPYNCLSNPEEILLDGERISTGNSSIDI-----SLSLVQL	44
QY	54	VGTVSSFLKKVGLSIGKRIILSELWGLIFPSPGNTNMQDILIRETEQFLNQRLNTDTLARV	113
DB	45	L--VSNF-VPGGGFLVG--LLDFVWGIVGSPSP---WDAFLVQIEQLINERIAAAYSAA	95
QY	114	NAELEGLOANIREFNQOVDNELN---PTQNPVPLS-ITSSVNTMQQLFLNRLPQFRVQY	169
DB	96	ISNLEGLGN---FNIYVEAFKEWEADPDNPVTRRVVDREFILDGLLERDIPSFRIAGF	152
QY	170	QLLLPLPFAQAAMHLSFIRDVVLNADEWGISAAATLRTYQNVLYKNVYTEYSNYCINTYQT	229
DB	153	EVPLL SVYAQAANLHLAILRDSIFGARWGGLTTINVNENYNRLIRHIDEYANHCADTYN-	211
QY	230	AFRGLN-----TRLHDMLEF-----RTYMFNLNVFEYVSIWSLFKYQSLLVSSGANL----	278
DB	212	--RGLNNLPKSTQYDWTYNRLFRDLTTLVDIAAFFPSPYDNRRYPYIQSVGQLTREIYTD	269

QY	279	--GSGPQ----	QTQSFTSQD-----	WPLYSL-----	FQVNSNYVLNGFSGAR	311
Db	270	PLITFPQLQVAQLPTFNVMESNAIRTPHLFDVLNLTIFTDWFSVGRNFYWGG-----	324			
QY	316	LTQTFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAVFNQ-----	NFSCS-----	TFLP	366	
Db	325	-----HRVISNRIG-GGNITSPIYGREANQEPPRSFTFNGPVFRTLSN	366			
QY	367	PLLTPEVRSWLDSGDRGGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDYFIRNIS	426			
Db	367	PTEFRLQQWPAPPFNLRVEGV-----	EFTPL-----	NSFTYRGRGT-----	VDSLTLT	410
QY	427	GVP-----LVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIY--	AVHE-	478		
Db	411	ELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTTPGVFSWTHRSATDRNIIPDVINOI	470			
QY	479	-----NGTMILAPEDYTGFTTISPIHATOVANNQTRTFISEKEFGNQGDSLRFEQSNT	529			
Db	471	PLVKAFNLTSGTSVVRGP---GFTGGDIIRTNVNGSVLSM-----	SLNF--SNT	514		
QY	530	TARYTLRGNGNSYLVLRVSSLGNSTIRVTINGRVYTASNVTNTTNDG-----	VNDNGA-	584		
Db	515	TLQ-----RYRVRVRYAASQTMVMMSVTVGG-----	STTGNOGFPPSTMANGAL	557		
QY	585	-----REFLDINMGNVVASDNTNVPLDINTVFNSGTQ-FELMMIMFVP	625			
Db	558	TSQSFRFAEFPVG-ISASCSQGA--SISISNNVGRQMFLDRIEFLP	601			

RESULT 11

parasporal crystal protein - *Bacillus thuringiensis* (strain aizawai IPL7)
N/Alternate names: 135K insecticidal protein
C/Species: *Bacillus thuringiensis*
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Dec-2000
C/Accession: JT0241
R/Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
Agric. Biol. Chem. 52, 1565-1573, 1988
A/Title: Cloning and expression in *Escherichia coli* of the 135-kDa insecticidal protein
A/Reference number: JT0241
A/Accession: JT0241
A/Molecule type: DNA
A/Residues: 1-1176 <SHI>
A/Note: b. *thuringiensis* aizawai IPL7 produces similar 130K and 135K insecticidal proteins
C/Comment: The 135K protein has insecticidal activity against *Plutella xylostella* larvae
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 8.5%; Score 282.5; DB 2; Length 1176;
Best Local Similarity 21.7%; Pred. No. 5.2e-11;
Matches 152; Conservative 105; Mismatches 271; Indels 173; Gaps 29;

QY 6 NNGRTTICDAYNVVAHDFFSEHKSLDTIRKEWMEWKRT--DHSLYVAPIVGTVSSFLLK 63
DB 3 NNPINECIPNCLS-----NPEVEVLGGERIETGYPIDISL-----SLTQFLLS 48
QY 64 K----VGSLLIGKRLSELWGLFFPSGSTNLMDILRETEQFLNQLNRLTDLARVNAELEG 119
DB 49 EFVPGAGFVLG--LVDDIIGIFGPS---QWDAFLVQIEQLINQRIEEFARNQAISRLEG 102
QY 120 LQ-----ANIREFNQQVDNFLNPTQNVPVLSITSSVNTMQQLFLNRLPQFRVQGYQLL 172
DB 103 LSNLYQIYAESFREWE-----ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP 156
QY 173 LLPLFAQAA NMHLSFIRDVVLNADEWGISAATLRTYQNYLKNYTTYSNVCINTYQTAFR 232
DB 157 LLSVYVQAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216
QY 233 ---GLNTRLHML---EFRTYMFNLNVEFYVSIWSLFKYQSLVSSGANLYASGSGPQQTQ 286
DB 217 RVWGPDSR--DWVRYNQFRRELTLTVLDIVALFS-----NYDSRRYPPIRTV 260
QY 287 SFTSQDWPFLYSLFQWNSNYVLNGFSGA-----RLTQTF--PNIGLPGCTTHALLAA 338

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Db 261 SQLTR-----EIYTNPVLENFDGSRGMAQRIEQNIRQPHLMDILNSITIYTDVHR 311
QY 339 RVNYSGG--VSSGDIGAVFNQNFSCSTF-----LPLLTP----- 371
Db 312 GFNYWSGHQITASPVG-----FSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPL 365
QY 372 FVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDYFIRNISGVPLV 431
Db 366 YRRIILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQGT-----VSLDVIIPPQ 417
QY 432 VRNEDLRRPLHY--NEIRNIESPSGTPGGLRAYMVSVHNRK--NNIYAVHE----- 478
Db 418 DNSVPPRAGFSHRLSHVTMLSQLAAGAVYTLRAPTFWSQHRSAEFNNIIPSSQITQIPLTK 477
QY 479 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRFESQNTTARY 533
Db 478 STNLGSGTSVVKGP---GFT-----GGDILR--RTSPGQIS 508
QY 534 TLRGN-----GNSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLD 588
Db 509 TLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSS--GSNLQSGSFRT 567
QY 589 INMGNVASDNTNVPLDINV--TFNSGTQFELMNMIMFVPTNL 628
Db 568 VGFTTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 608

RESULT 12
A22798
parasporal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 01-Dec-2000
C;Accession: A22798
R;Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A;Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thurin
A;Reference number: A22798; PMID:85232070; PMID:2989108
A;Accession: A22798
A;Molecule type: DNA
A;Residues: 1-934 <SHI>
A;Cross-references: GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713
C;Comment: The authors translated the codon ACA for residue 264 as Ser.
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 8.5%; Score 280.5; DB 2; Length 934;
Best Local Similarity 21.7%; Pred. No. 5.1e-11;
Matches 152; Conservative 104; Mismatches 272; Indels 173; Gaps 29;

QY 6 NNGRTTICDAYNVVAHDPFSFEHKS LDTIRKENWEWKRT--DHSLYVAPIVGTVSFLLK 63
Db 3 NNPINECIPYNCLSD-----NPEVEVLGGERIETGYTPIDISL-----SLTQFLLS 48
QY 64 K---VGS LIGKRILSELWGLIFPSGSTNLMDILRETEQFLNQRNLNTDILARVNAELEG 119
Db 49 EFVPGAGFVLG--LVDIWGIFGPS---QWDAPFLVQIEQLINQRIEFAFNQAISRLEG 102
QY 120 LQ-----ANIREFNQVDNFLNPTQNPVPLSITSSVNTMQQLFNLRLPQFRVQGYQLL 172
Db 103 LSNLYQIYAESFREWE-----ADPTNPALREEMRIQFNDMNSALTTAIFLFAVQNYQVP 156
QY 173 LLPLFAQAANMHLSFIRDVVLNADEWGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFR 232
Db 157 LLSVYVQAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216
QY 233 ---GLNTRLHMDL---EFRTYMFNLNVEYVSIWLSFKYQSLLVSSGANLYASGSGPQQTQ 286
Db 217 RWGPDNR--DWVRYNQFRRELTTLVLDIVALEF-----NYDSRRYPPIRTV 260
QY 287 SFTSQDWPFYLSLFQVNSNYVLNGFSGA-----RLTQTF--PNIGGLPGTTTHALLAA 338
Db 261 SQLTR-----EIYTNPVLENFDGSRGMAQRIEQNIRQPHLMDILNIRITIYTDVHR 311
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QY 339 RVNYSGG--VSSGDIGAVFNQNFSCSTF-----LPLLTP----- 371
Db 312 GFNYWSGHQITASPVG-----FSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPL 365
QY 372 FVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDYFIRNISGVPLV 431
Db 366 YRRIILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQGT-----VSLDVIIPPQ 417
QY 432 VRNEDLRRPLHY--NEIRNIESPSGTPGGLRAYMVSVHNRK--NNIYAVHE----- 478
Db 418 DNSVPPRAGFSHRLSHVTMLSQLAAGAVYTLRAPTFWSQHRSAEFNNIIPSSQITQIPLTK 477
QY 479 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRFESQNTTARY 533
Db 478 STNLGSGTSVVKGP---GFT-----GGDILR--RTSPGQIS 508
QY 534 TLRGN-----GNSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLD 588
Db 509 TLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSS--GSNLQSGSFRT 567
QY 589 INMGNVASDNTNVPLDINV--TFNSGTQFELMNMIMFVPTNL 628
Db 568 VGFTTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 608

RESULT 13
B42459
hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag
C;Species: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 30-Sep-1993
C;Accession: B42459
R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene fro
A;Reference number: A42459; PMID:91286178; PMID:2061280
A;Accession: B42459
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <CHA>
A;Cross-references: GB:M63897
C;Superfamily: parasporal crystal protein

Query Match 8.4%; Score 277.5; DB 2; Length 380;
Best Local Similarity 26.3%; Pred. No. 2.1e-11;
Matches 100; Conservative 66; Mismatches 135; Indels 79; Gaps 19;

QY 21 HDPFSFEHK-----SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKISEYENVEPVSASTIQTGISIAG 68
QY 53 -IVGTVSSFLKKGSLIGKRILSELWGLIFPSGSTNLMDILRETEQFLNQRNLNTDTLA 111
Db 69 KILGTGVFPFAGQVASLY-SFILGELW----PKGK-NQWEIFMEHVEEIIINQKISTYARN 122
QY 112 RVNAELEGLOQANIREFNQVDNFLNPTQNPVPLSIT--SSVNTMQQLFNLRLPQFRVQGYQ 170
Db 123 KALTDLKGLDALAVYHESLESWVGNRKNTRARSVVKVKSQYIALELMFVQKLPSFAVS GEE 182
QY 171 LLLLPLFAQAANMHLSFIRDVVLNADEWGISAATLRTYQNYLKNYTTTEYSNYCINTYQTA 230
Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYS DHCVKWYSTG 242
QY 231 FRGL-NTRLHMDL---EFRTYMFNLNVEYVSIWLSFKYQSLLVSSGANL-----YASGS 280
Db 243 LNNLRGTNAESWVRYNQFRKDMTLMVLDLVALFP--SYDTLVYPIKTTSQLTREVTDAI 300
QY 281 GP-QQTSQTSQDW-----PFL-----YSLFQVNSN-YVLNGF 311
Db 301 GTVHPNASPASTTWYNNNAPSFTSTIESAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
QY 312 SGARLTQTFPNIGGLPGTTT 331
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Sat Dec 16:14:54 2003

us-10-040a-2.rpr

Page 9

Search completed: December 12, 2003, 16:18:10
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:16:21 ; Search time 36 Seconds
(without alignments)
3265.046 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
Sequence: 1 MNVNLNNGRTTICDAYNVVA.....GTQFELMNIMFVTNLPPYIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3314	100.0	632	12	US-10-040-906A-2
2	3309	99.8	633	12	US-10-040-906A-8
3	3120	94.1	632	12	US-10-040-906A-4
4	3043.5	91.8	634	12	US-10-198-478-12
5	3043.5	91.8	634	12	US-10-102-469-18
6	3010.5	90.8	633	12	US-10-198-478-18
7	3005.5	90.7	634	12	US-10-198-478-2
8	2523.5	76.1	627	12	US-10-040-906A-6
9	311.5	9.4	1156	15	US-10-099-285-72
10	305.5	9.2	643	9	US-09-826-660-25
11	305.5	9.2	1186	9	US-09-826-660-23
12	282.5	8.5	609	12	US-10-107-581-8
13	280.5	8.5	609	12	US-10-107-581-7
14	276.5	8.3	609	12	US-10-107-581-5
15	276.5	8.3	609	12	US-10-107-581-6

16	275.5	8.3	1207	11	US-09-988-462-7	Sequence 7, Appli
17	272	8.2	1177	15	US-10-035-060-6	Sequence 6, Appli
18	271.5	8.2	609	12	US-10-107-581-3	Sequence 3, Appli
19	271.5	8.2	609	12	US-10-107-581-4	Sequence 4, Appli
20	269.5	8.1	667	12	US-10-414-637-8	Sequence 8, Appli
21	269.5	8.1	667	14	US-10-032-717-8	Sequence 8, Appli
22	269.5	8.1	673	12	US-10-414-637-18	Sequence 18, Appl
23	269.5	8.1	673	14	US-10-032-717-18	Sequence 18, Appl
24	269.5	8.1	1210	12	US-10-414-637-4	Sequence 4, Appli
25	269.5	8.1	1210	14	US-10-032-717-4	Sequence 4, Appli
26	268	8.1	615	12	US-10-102-469-8	Sequence 8, Appli
27	268	8.1	617	12	US-10-137-682A-1	Sequence 1, Appli
28	268	8.1	1155	9	US-09-756-643-2	Sequence 2, Appli
29	268	8.1	1155	11	US-09-988-462-9	Sequence 9, Appli
30	268	8.1	1177	12	US-10-102-469-24	Sequence 24, Appl
31	268	8.1	1181	11	US-09-988-462-11	Sequence 11, Appl
32	268	8.1	1181	11	US-09-988-462-13	Sequence 13, Appl
33	268	8.1	1181	11	US-09-988-462-15	Sequence 15, Appl
34	268	8.1	1181	11	US-09-988-462-17	Sequence 17, Appl
35	268	8.1	1181	11	US-09-988-462-28	Sequence 28, Appl
36	267.5	8.1	1178	9	US-09-851-194-2	Sequence 2, Appli
37	266.5	8.0	1178	12	US-10-102-469-10	Sequence 10, Appl
38	266.5	8.0	1178	12	US-10-102-469-12	Sequence 12, Appl
39	266.5	8.0	1178	12	US-10-102-469-14	Sequence 14, Appl
40	266	8.0	1177	15	US-10-035-060-2	Sequence 2, Appli
41	265	8.0	605	9	US-09-826-660-4	Sequence 4, Appli
42	265	8.0	1148	9	US-09-826-660-2	Sequence 2, Appli
43	265	8.0	1174	9	US-09-826-660-6	Sequence 6, Appli
44	265	8.0	1177	9	US-09-873-873-34	Sequence 34, Appl
45	265	8.0	1177	12	US-10-365-645-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-10-040-906A-2
; Sequence 2, Application US/10040906A
; Publication No. US20030167517A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Van Houdt, Sara
; TITLE OF INVENTION: No. US20030167517A1el Bacillus thuringiensis insecticidal protein
; FILE REFERENCE: 58764.000036
; CURRENT APPLICATION NUMBER: US/10/040.906A
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-040-906A-2

Query Match	100.0%;	Score 3314;	DB 12;	Length 632;
Best Local Similarity	100.0%;	Pred. No. 1.4e-293;		
Matches 632;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNVNLNNGRTTICDAYNVVAHDPFSEHKSLDITIRKEWMEWKRTDHSLYVAPIGTVSSP	60	
Db	1	MNVNLNNGRTTICDAYNVVAHDPFSEHKSLDITIRKEWMEWKRTDHSLYVAPIGTVSSP	60	
QY	61	LLKVGSLIGKRILSELWGLIFPSGSTNLMDILRETEQFLNQLNTDTLARVNAEGL	120	
Db	61	LLKVGSLIGKRILSELWGLIFPSGSTNLMDILRETEQFLNQLNTDTLARVNAEGL	120	
QY	121	QANIREFNQVDNPNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA	180	
Db	121	QANIREFNQVDNPNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA	180	

QY 181 ANMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAVFNQNF 360
Db 301 QVNSNYVLNGFSGARLTQTFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAVFNQNF 360
QY 361 CSTFLPPLLTPFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPDY 420
Db 361 CSTFLPPLLTPFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPDY 420
QY 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
QY 481 TMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQSNNTTARYTLRGNGN 540
Db 481 TMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQSNNTTARYTLRGNGN 540
QY 541 SYNLYLRVSSLGNSTIRVTINGRVTASNVNTTTNNDGVNDNGARFLDINMGVNVASDNT 600
Db 541 SYNLYLRVSSLGNSTIRVTINGRVTASNVNTTTNNDGVNDNGARFLDINMGVNVASDNT 600
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Db 601 NVPLDINVTFNSGTQFELNMIMFVPTNLPPYY 632

RESULT 2

US-10-040-906A-8
; Sequence 8, Application US/10040906A
; Publication No. US20030167517A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Van Houdt, Sara
; TITLE OF INVENTION: No. US20030167517A1el Bacillus thuringiensis insecticidal protein
; FILE REFERENCE: 58764.000036
; CURRENT APPLICATION NUMBER: US/10/040,906A
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial Sequence
US-10-040-906A-8

Query Match 99.8%; Score 3309; DB 12; Length 633;
Best Local Similarity 100.0%; Pred. No. 4e-293;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSFL 61
Db 3 NNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSFL 62
QY 62 LKKVGSLLIGKRIILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLARVNAEGLQ 121
Db 63 LKKVGSLLIGKRIILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLARVNAEGLQ 122
QY 122 ANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQAA 181
Db 123 ANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQAA 182

QY 182 NMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 241
Db 183 NMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 242
QY 242 LEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLFQ 301
Db 243 LEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLFQ 302
QY 302 VNSNYVLNGFSGARLTQTFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAVFNQNF 361
Db 303 VNSNYVLNGFSGARLTQTFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAVFNQNF 362
QY 362 STFLPPLLTPFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPDY 421
Db 363 STFLPPLLTPFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPDY 422
QY 422 IRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 481
Db 423 IRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 482
QY 482 MIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQSNNTTARYTLRGNGNS 541
Db 483 MIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQSNNTTARYTLRGNGNS 542
QY 542 YNLYLRVSSLGNSTIRVTINGRVTASNVNTTTNNDGVNDNGARFLDINMGVNVASDNTN 601
Db 543 YNLYLRVSSLGNSTIRVTINGRVTASNVNTTTNNDGVNDNGARFLDINMGVNVASDNTN 602
QY 602 VPLDINVTFNSGTQFELNMIMFVPTNLPPYY 632
Db 603 VPLDINVTFNSGTQFELNMIMFVPTNLPPYY 633

RESULT 3

US-10-040-906A-4
; Sequence 4, Application US/10040906A
; Publication No. US20030167517A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Van Houdt, Sara
; TITLE OF INVENTION: No. US20030167517A1el Bacillus thuringiensis insecticidal protein
; FILE REFERENCE: 58764.000036
; CURRENT APPLICATION NUMBER: US/10/040,906A
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-040-906A-4

Query Match 94.1%; Score 3120; DB 12; Length 632;
Best Local Similarity 93.4%; Pred. No. 7.2e-276;
Matches 590; Conservative 27; Mismatches 15; Indels 0; Gaps 0;
QY 1 MNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDTRKEWMEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNSVLNSGRTTICDAYNVVAHDPPSFQHKSLDTIQEEMWEWKDNHSLYVDPVIGTVASF 60
QY 61 LKKVGSLLIGKRIILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLARVNAEGL 120
Db 61 LKKVGSLLIGKRIILSELNRLNLFPSGNTLMQDILRETEKFLNQLRNTDTLARVNAELTGL 120
QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNLFNPNRNVPLSITSSVNTMQQLFLNRLTQFQMGYQLLLPLFAQA 180
QY 181 ANMHLSFIRDVVLNADWEGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240



Db 181 ANLHLSFIRDVILNADWEGISAATLRTYQNHRLNRYTRDYSNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFSTQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFSTQDWPFLYSLF 300
QY 301 QVNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNSYGGVSSGDIGAVFNQFNS 360
Db 301 QVNSNYVLNGFSGARLTQTFFPNIVGLPGTTTTTHALLAARVNSYGGVSSGDIGAVFNQFNS 360
QY 361 CSTFLPPLLTFFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDY 420
Db 361 CSTFLPPLLTFFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDY 420
QY 421 FTRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 421 FTRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
QY 481 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNTTARYTLRGNGN 540
Db 481 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNTTARYTLRGNGN 540
QY 541 SYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDNT 600
Db 541 SYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNVVASDNT 600
QY 601 NVPLDINVTFNSGTQFELNMIMFVPTNLPIY 632
Db 601 NVPLDINVTLNSGTQFELNMIMFVPTNISPLY 632
RESULT 4
US-10-198-478-12
; Sequence 12, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 634
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: an amino acid sequence encoded by a completely synthesized nucle
; OTHER INFORMATION: tide sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(634)
; OTHER INFORMATION:
US-10-198-478-12
Query Match 91.8%; Score 3043.5; DB 12; Length 634;
Best Local Similarity 90.7%; Pred. No. 7e-269;
Matches 573; Conservative 34; Mismatches 24; Indels 1; Gaps 1;
QY 2 NNVLNNGRTTICDAYNVVAHDPPSFHEKSLDITIRKEWMEWKRTDHSLYVAPIVGTVSSFL 61
Db 3 NNVLNNGRTTICDAYNVVAHDPPSFHEKSLDITIRKEWMEWKRTDHSLYVAPIVGTVSSFL 62
QY 62 LKKVGSGLIGKRIKILSELWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEGLO 121
Db 63 LKKVGSGLIGKRIKILSELWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEGLO 122
QY 122 ANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFIQGYQLLLPLPAQAA 181

Db 123 ANIREFNQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFIQGYQLLLPLPAQAA 182
QY 182 NMHLSFIRDVILNADWEGISAATLRTYQNYLKNYTYTEYSNYCINTYQTAFRGLNTRLHDM 241
Db 183 NMHLSFIRDVILNADWEGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDM 242
QY 242 LEFRTYMFNLVFEYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFSTQDWPFLYSLFQ 301
Db 243 LEFRTYMFNLVFEYVSIWSLFKYQSLMVSSGANLYASGSGPQQTQSFSTQDWPFLYSLFQ 302
QY 302 VNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNSYGGVSSGDIGAV-FNQFNS 360
Db 303 VNSNYILSGISGTRLSITFPNIGGLPGSTTTTHSLNSARVNSYGGVSSGLIGATNLNHNEN 362
QY 361 CSTFLPPLLTFFVRSWLDGSDRGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDY 420
Db 363 CSTVLPPLSTPFVRSWLDGSDTREGVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPDY 422
QY 421 FIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 423 FIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYLVSVHNRKNNIYAAENG 482
QY 481 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNTTARYTLRGNGN 540
Db 483 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQSNTTARYTLRGNGN 542
QY 541 SYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDNT 600
Db 543 SYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTTNDGVNDNGARFSDINIGNIVASDNT 602
QY 601 NVPLDINVTFNSGTQFELNMIMFVPTNLPIY 632
Db 603 NVPLDINVTLNSGTQFELNMIMFVPTNLPLY 634
RESULT 5
US-10-102-469-18
; Sequence 18, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; APPLICANT: Perlak, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 634
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding P2 insecticidal protein
US-10-102-469-18
Query Match 91.8%; Score 3043.5; DB 12; Length 634;
Best Local Similarity 90.7%; Pred. No. 7e-269;
Matches 573; Conservative 34; Mismatches 24; Indels 1; Gaps 1;
QY 2 NNVLNNGRTTICDAYNVVAHDPPSFHEKSLDITIRKEWMEWKRTDHSLYVAPIVGTVSSFL 61
Db 3 NNVLNNGRTTICDAYNVVAHDPPSFHEKSLDITIRKEWMEWKRTDHSLYVAPIVGTVSSFL 62
QY 62 LKKVGSGLIGKRIKILSELWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEGLO 121

Db 63 LKKVGLIGKRILSELWGIIFFSGSTNLMQDILRETEQFLNQRINTDTLARVNAELIGLQ 122
Qy 122 ANIREFNOQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQAA 181
Db 123 ANIREFNOQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFIQGYQLLLPLFAQAA 182
Qy 182 NMHLSFIRDVVLNADEWGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHDM 241
Db 183 NMHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDM 242
Qy 242 LEFRTYMFNLNVEFYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLFQ 301
Db 243 LEFRTYMFNLNVEFYVSIWSLFKYQSLMVSSGANLYASGSGPQQTQSFTAQNWPFYLSLFQ 302
Qy 302 VNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGAV-FNQNFS 360
Db 303 VNSNYVLNGFSGARLTQTFFPNIGGLPGSTTTTHLSNSARVNYSGGVSSGLIGATNLNHNFN 362
Qy 361 CSTFLPPLLTPFVRSWLDGSDRGGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPDY 420
Db 363 CSTVLPPLSTPFVRSWLDGSDRGVATSTNWQTESFOTLSLRCGAFSARGNSNYFPDY 422
Qy 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 423 FIRNISGVPLVVRNEDLRPLHYNQIRNIESPSGTPGGARAYLVSVHNRKNNIYAAENG 482
Qy 481 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTTARYTLRGNG 540
Db 483 TMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTTARYTLRGNG 542
Qy 541 SYNLYLRVSSLGNSSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDNT 600
Db 543 SYNLYLRVSSIGNSSTIRVTINGRVYTVSNVNTTNTNDGVNDNGARFSDINIGNIVASDNT 602
Qy 601 NVPLDINVTNFSGTQFELMNMIMFVPTNLPPY 632
Db 603 NVPLDINVTNLSGTQFELMNMIMFVPTNLPLY 634

RESULT 6
US-10-198-478-18
; Sequence 18, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-198-478-18

Query Match 90.8%; Score 3010.5; DB 12; Length 633;
Best Local Similarity 89.7%; Pred. No. 7.2e-266;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;
Qy 1 MNVNLNNGRTTICDAYNVVAHDPPFSFEHKSLSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSF 60
Db 1 MNSVLNSGRTTICDAYNVVAHDPPFSFQHKSLDVTQKEWTEWKNNHSLYLDPIVGTVASF 60
Qy 61 LLKKVGLIGKRILSELWGIIFFSGSTNLMQDILRETEQFLNQRINTDTLARVNAELEG 120
Db 61 LLKKVGLVIGKRILSELNLIFPSGSTNLMQDILRETEKFLNQRINTDTLARVNAELTGL 120

Qy 121 QANIREFNOQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLPLFAQA 180
Qy 181 ANMHLSFIRDVVLNADEWGISAATLRTYQNYLKNYTTTEYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANLHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQSAFGLNTRLHD 240
Qy 241 MLEFRTYMFNLNVEFYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLF 300
Db 241 MLEFRTYMFNLNVEFYVSIWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTFFPNIGGLPGTTTTTHALLAARVNYSGGVSSGDIGA-VFNQNF 359
Db 301 QVNSNYVLNGFSGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGGISSGDIGASPFNQNF 360
Qy 360 SCSTFLPPLLTPFVRSWLDGSDRGGVNTVTNWQTESFESTLGLRCGAFARGNSNYFPD 419
Db 361 NCSTFLPPLLTPFVRSWLDGSDRGVATVTNWQTESFETTLGLRSGAFARGNSNYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHAVHEN 480
Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTTARYTLRGNG 539
Db 481 GSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNNTTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLGNSSTIRVTINGRVYTASNVTNTTNDGVNDNGARFLDINMGNVVASDN 599
Db 541 NSYNLYLRVSSIGNSSTIRVTINGRVYTATNVNTTNTNDGVNDNGARFSDINIGNIVASSN 600
Qy 600 TNVPLDINVTNFSGTQFELMNMIMFVPTNLPPY 632
Db 601 SDVPLDINVTNLSGTQFELMNMIMLVPTNISPLY 633

RESULT 7
US-10-198-478-2
; Sequence 2, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 634
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: an amino acid sequence encoded by a completely synthesized nucleo
; OTHER INFORMATION: tide sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(634)
; OTHER INFORMATION:
US-10-198-478-2

Query Match 90.7%; Score 3005.5; DB 12; Length 634;
Best Local Similarity 89.7%; Pred. No. 2.1e-265;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;
Qy 2 NNVLNNGRTTICDAYNVVAHDPPFSFEHKSLSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSFL 61
Db 3 NSVLNSGRTTICDAYNVVAHDPPFSFQHKSLDVTQKEWTEWKNNHSLYLDPIVGTVASFL 62



APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-099-285-72

Query Match 9.4%; Score 311.5; DB 15; Length 1156;
Best Local Similarity 23.3%; Pred. No. 5.5e-19;
Matches 157; Conservative 96; Mismatches 221; Indels 199; Gaps 32;

QY 52 PIVGTSSFLKVKVGLIGKRIKILSELWGLIFPSGSTNLMQDILRETEQFLNQLRNTDTLA 111
Db 87 PFGQIVSFY-----QFLNLTW---PVNDTAIWEAFMRQVEELVNOQITEFARN 133

QY 112 RVNAELEGLOANIREFNQVDNLF--NPTQNPVPLSITSSVNTMQQL-FLNRLPQFRVQ 167
Db 134 QALARLOGLGDSFNVYQSLQNLWADRNDTRN--LSVVRAQFIALDLDFVNAIPLFAVN 190

QY 168 GYQLLLPLFAQAANMHLFIRDVVLNADWEGISAATLRTYQNYLKNYTYEYSNYCINTY 227
Db 191 GQQVPLLSVYAQAANLHLLKLDASLFGGEGWGFTQGEISTYDRQLELTAKYNYCETWY 250

QY 228 QTA---FRGLNT---RLHDMLEFRTYMFNLFVFEVYSIWSLFKYQSLVSSGANLYASGS 280
Db 251 NTGLDRLRGNTTESWLRH---QFRREMTLVLDV---ALFPYYDV-----RLYPTGS 298

QY 281 GPQQTQS-FTS-----QDW-----QDLY-----PFLY-----S 298
Db 299 NPQLTREYVTDPIVENPPANVGLCRRWGTPNYNPFSELENAFIRPPHLFDRNLSTISSN 358

QY 299 LFQVNSNYVLNGFSGARLTQTFPNIGLPG-----TTTHALLAARVNSYSGVSSGDIG- 352
Db 359 RFPVSSNF-MDYWSGHTLRRSYLNDLSAVQEDSYGLITTTTRATINPGVDGNTRIESTAVDF 417

QY 353 ----AVFNQNFSCSTFLPPLLTFFVRSWLDSGD---RGVNTV--TNWQTESFESTLG 402
Db 418 RSALIGIYGVN-----RASFPVGGFLFNGTISPANGGCRDLYDTNDELPPDEST-- 465

QY 403 LRCGAFTARGNSNYFPDY-----FIRNISGVPLV---RNEDLRRPLHYNEIRNIESPS 453
Db 466 ---GSSTHRLSHVTFPSFQTNQAGSIANAGSVPTYVWTRRDVLDLNNITFPNRITQLP--- 519

QY 454 GTPGGLRAYMVSVHNRKNNIYAVHENGTMHILAPEDYTGFTTISPIHATQVNNQTRTFISE 513
Db 520 -----LVKA-----SAPVSGTTVLKGP-----GFT----- 539

QY 514 KFGNQGDSLRFEQSNNTARYTLRGNNS-----YNLYLRVSSLGNSSTIRVTINGRVYTAS 568
Db 540 ---GGGILRRITNGTFG--TLRVTVNSPLTQRYRVRVRFASSGNFSIRI-LRGNTSIAY 592

QY 569 NVNTTTNNDGVNDNGARFLDINMGNVVASDNTNVPLDINVTFF-----NSGT 614
Db 593 QRFEGSTMNRG-----QELTYESFVTSEFTTNQSDLPFTTQQAQENLTILAEGVSTGS 644

QY 615 QFELNMIMFVPTN 627
Db 645 EYFIDRIEIIIPVN 657

US-09-826-660-25
Sequence 25, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 643
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match 9.2%; Score 305.5; DB 9; Length 643;
Best Local Similarity 22.5%; Pred. No. 7.8e-19;
Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;

QY 52 PIVGTSSFLKVKVGLIGKRIKILSELWGLIFPSGSTNLMQDILRETEQFLNQLRNTDTLA 111
Db 73 PFAGQIASFYSFLVG-----ELW---PRG-RDPWEIFLEHVEQLIRQQVTENTRD 118

QY 112 RVNAELEGLOANIREFNQVDNLFNPTQNPVPLSITSSVNTMQQL-FLNRLPQFRVQYQ 170
Db 119 TALARLOGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQE 178

QY 171 LLLLPLFAQAANMHLFIRDVVLNADWEGISAATLRTYQNYLKNYTYEYSNYCINTYQTA 230
Db 179 VPLLWVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRQVKEKREYSYDVCARWYNTG 238

QY 231 FRGL-NTRLHDML--EERTYMFNLFVFEVYSIWSLFKYQSLVSSGANL---YASGSGP 282
Db 239 LNNLRGTNAESWLRYNQFRRDLTLGLVDLVALFSPSYDTRVYPMNTSAQLTREIYTDPIGR 298

QY 283 QQTQS-FTSQDWPFPLYSLFQVNSNYVLNGFSGARLTQTF-PNIGGLPGLTTTHALLAARV 340
Db 299 TNAPSGFASTNW-----FNNN--APSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWS 348

QY 341 NYSGGVSSGDIGAVFNQNFSCSTFLPPLTTPFVRSW---LDGSDRGGVNTVTN----- 391
Db 349 N-----TQYMNWVGHRLSRTIRGSLSTSTHGNTNT 380

QY 392 -----WQTESFES-----TLGLRCGAFTARGNSNYFPDYFIRNI--SG 427
Db 381 SINPVTLOFTSRDVYRTESFAGINILLTTPVNGVPWARFNWRNPLNLSRGLSLTYTIGYTG 440

QY 428 VPLVVRNEDLRRPLHYNEIRNIESPSCPTGGLRAYMVSVHNRKNNIYA-VHENGTMHILA 486
Db 441 VGTQLFDSETELPPETTERPNYESYSHRLSNIR--LISGNTLRAPVYSWTHRSA----- 492

QY 487 PEDYTGTISPITHATQVN-----NQTRTFISEKFGNQGDSLRFEQSNNTARYTLRNG 539
Db 493 --DRTN-TISSDSITQIPLVKSFNLNSGTSVVSFGPTGGDIIRTNVNGSVLSMGLNFNN 549

QY 540 NS---YNLYLRVSSLGNSSTIRVTING-RVYTASNVTNTTNDGVNDNGARFLDINMGNVV 595
Db 550 TSLQRYRVRVRYAASQTMVLRVTVGSGSTTFDQGFPPSTMSANESLTSQSFRFAEPVVGISA 609

QY 596 ASDNTNVPLDINVTNFSGTQ-FELNMIMFVP 625

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